

BEST AVAILABLE COPY

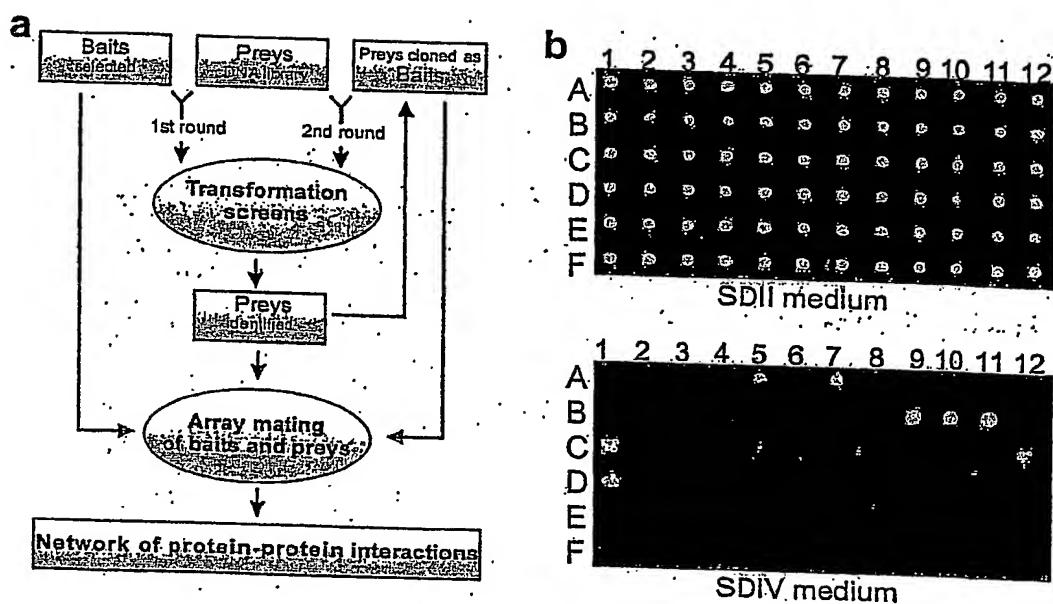
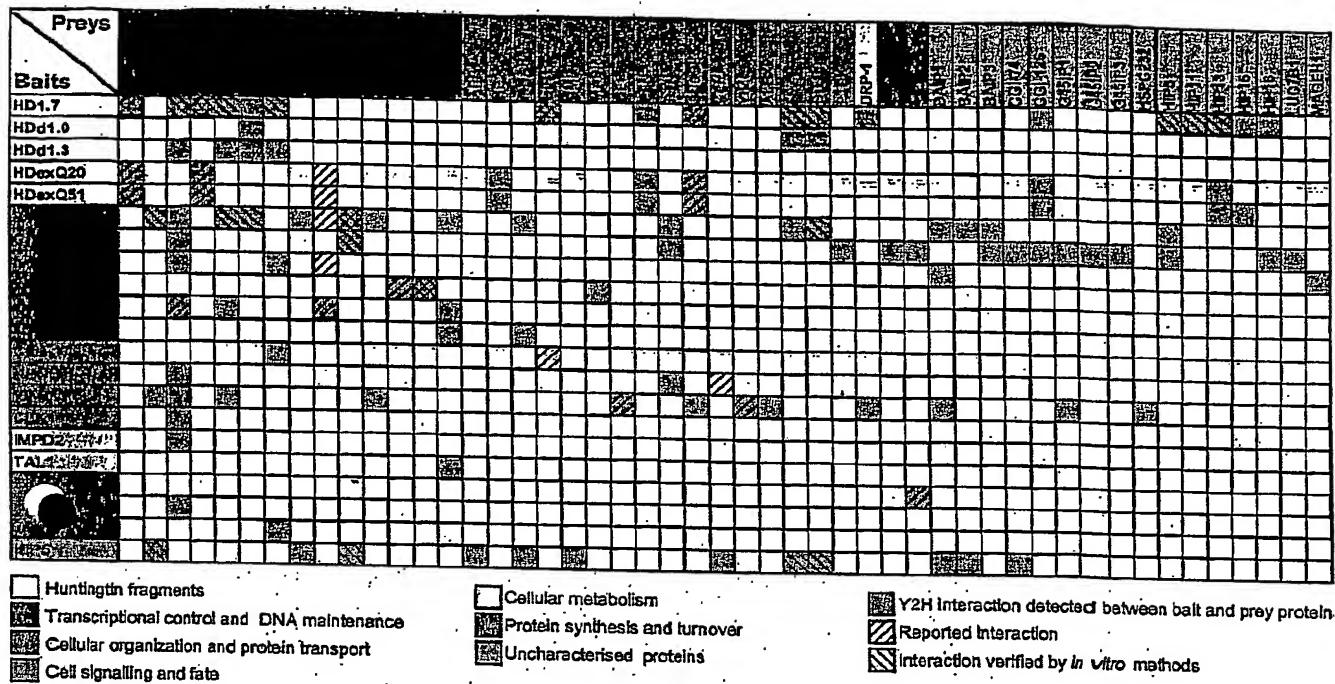


Figure 1

BEST AVAILABLE COPY

a



b

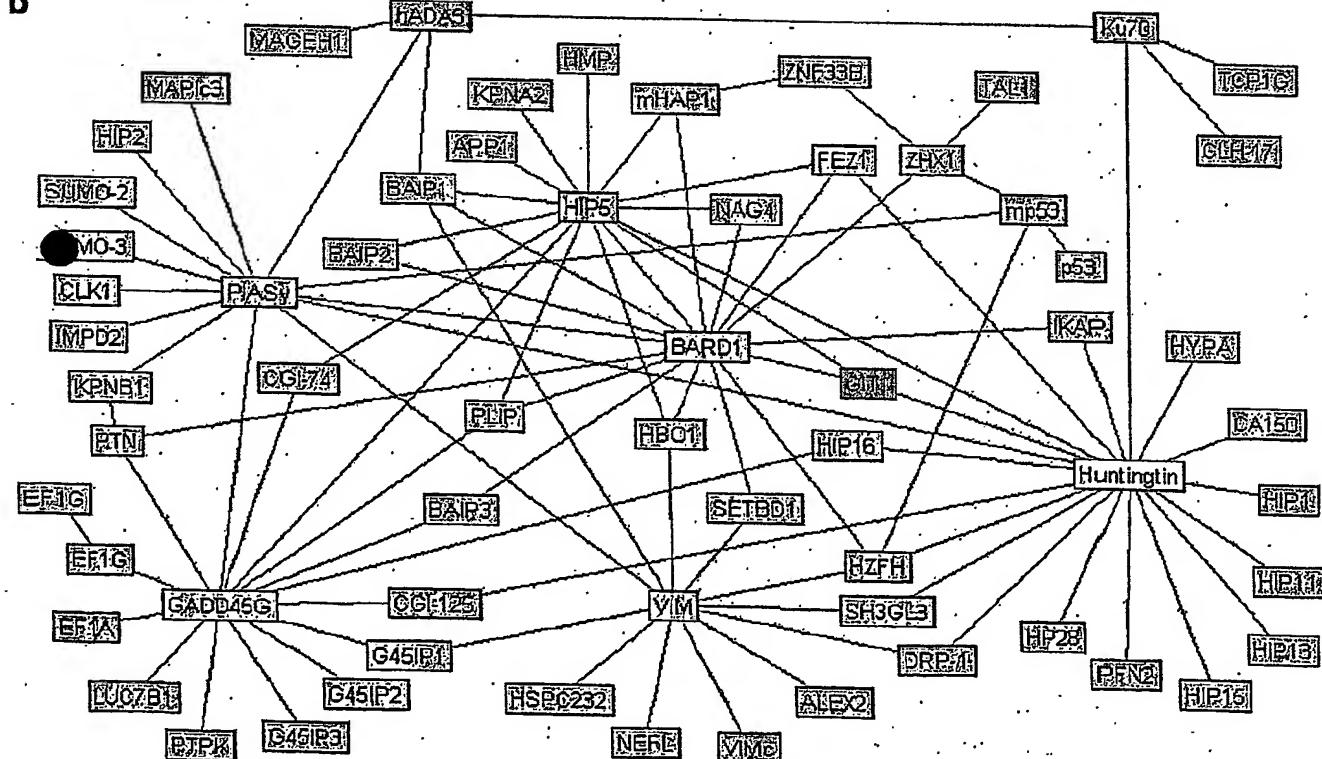


Figure 2

BEST AVAILABLE COPY

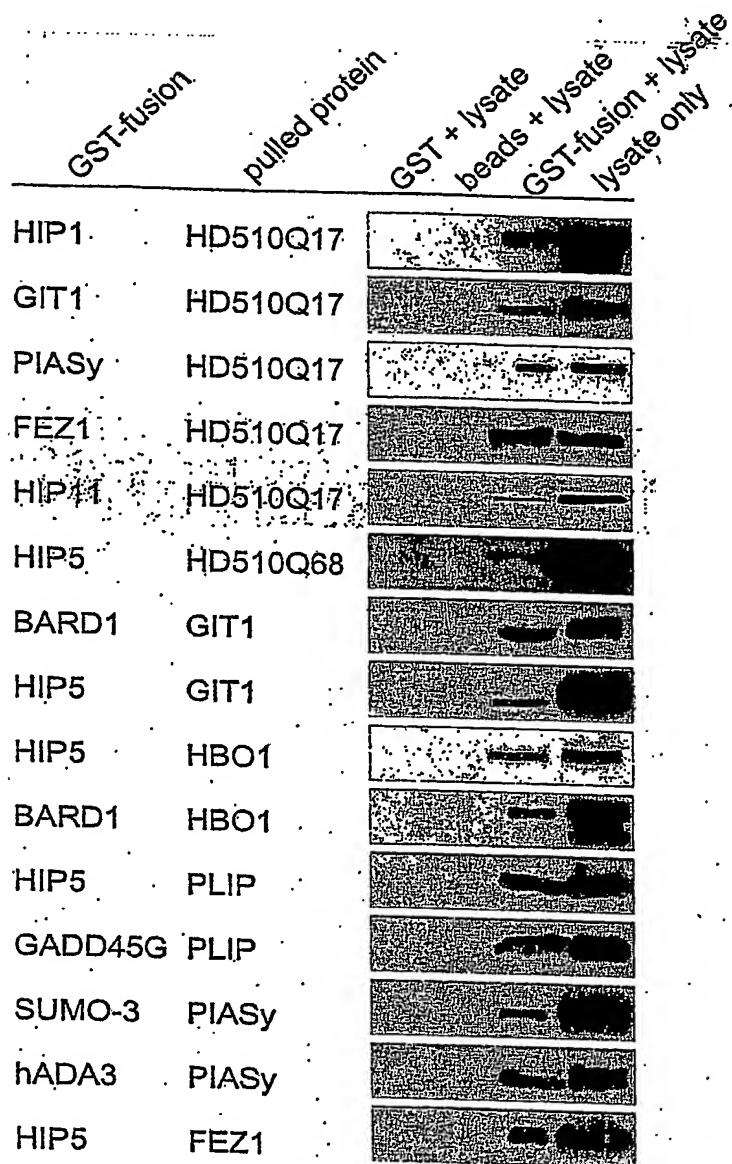


Figure 3

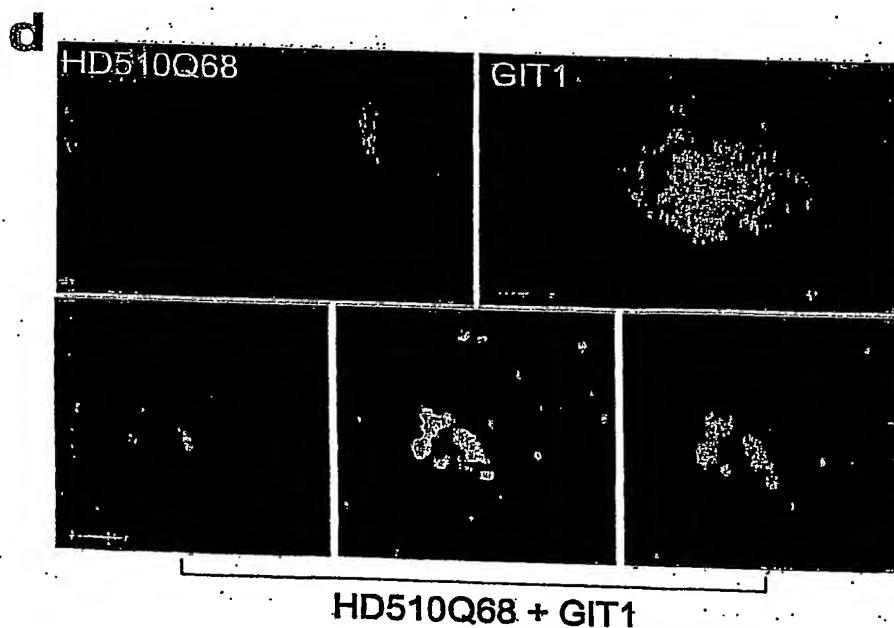
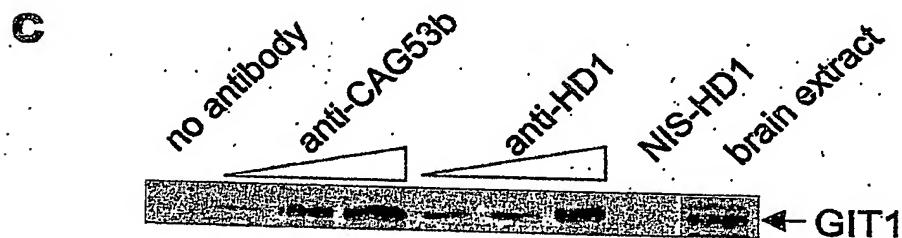
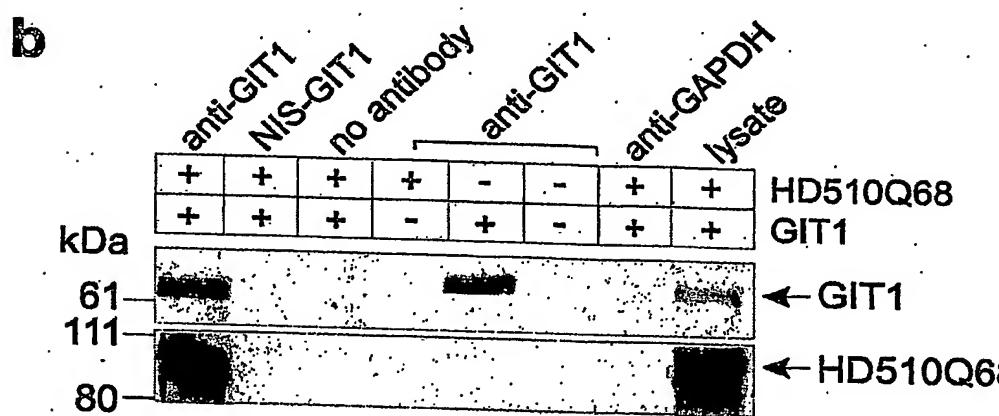
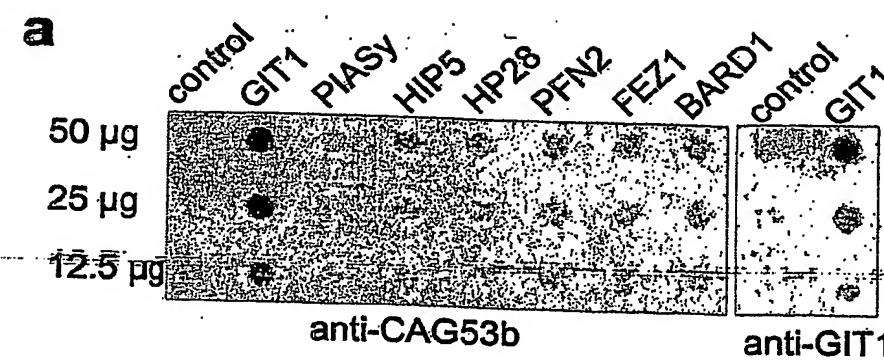
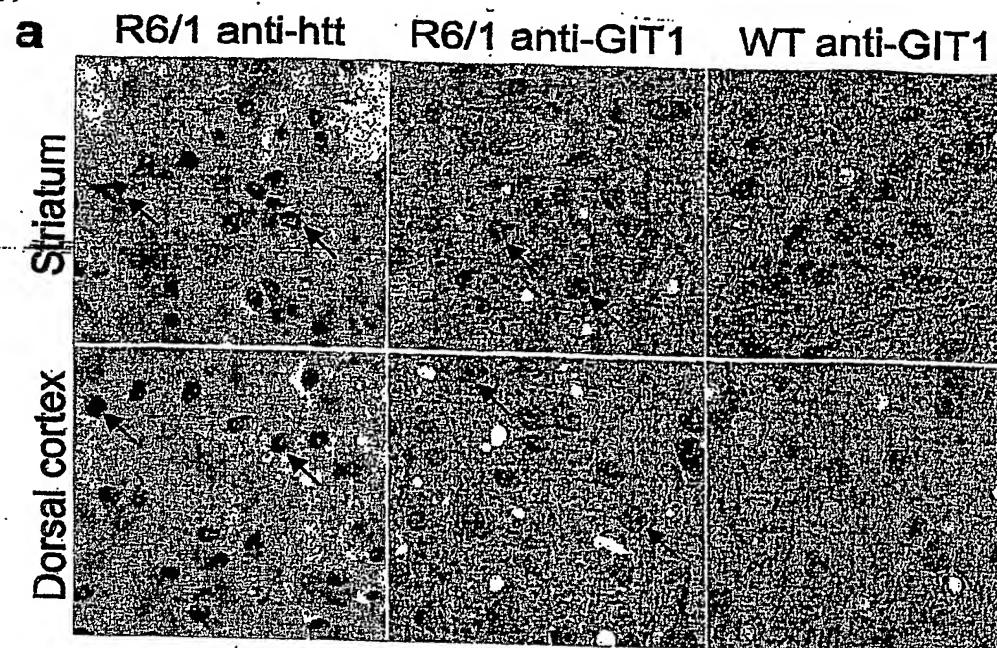


Figure 4



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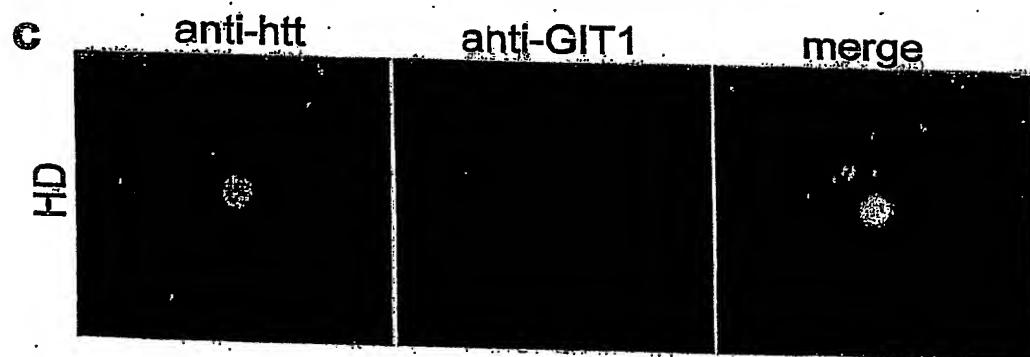
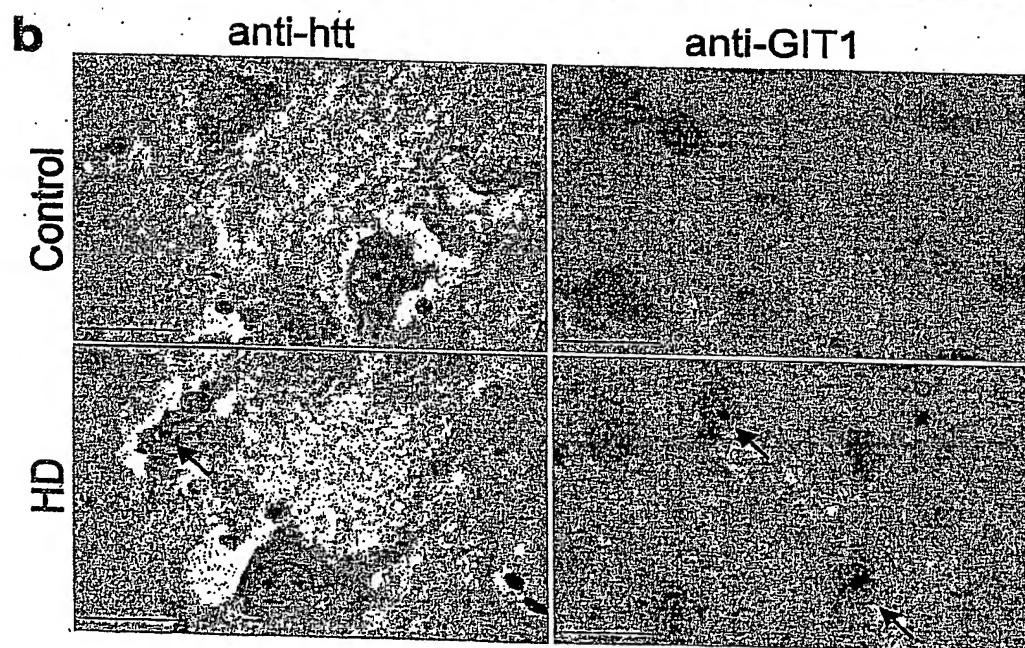


Figure 5

>ALEX2
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 ANGQOAFALAEVDPSEEGESGWTDTESDSDSEPETQRRGRGPVAMQKRPPYEDIDEILGVRDLRK
 VLALLQKSDDPFIQVALLTLSNNANYSNQETIRKLGGPLTIANMINKTDPHIKEKALMAMNNLS
 ENYENQCRQVYMNKVMDDITMASNINSAVQVVGKFLTNMTITNDYQHLLVNSIANFFRILSQGGG
 KIKVEILKILSNFAENPDMLKKLLSTQVPAFSSLVNSYVESEILINALTLFEIYDNLRAEVFNY
 REFNKGSLFYLCITTSQCVKKIRALANHHDLLVKVKVIKLNUKF
 >APP1
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 GFLRAKMDLEERRMROINEVMREWAMADNOSKNLPKADROALNEHFQSILOQTLERQVSGERQRLVE
 THATRVIALLNDQRRRALEGFLAALQADPQAEVLLALRRYLRAEQKEQRHTLHYQHVAADVPE
 KAQQMRFQVHHLQVIEERVNQSLGLLDQNPHLAQELRPQIQELLHSEHGPSELEAPAGGSSED
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 >BAIP1
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 LKKGRGQKEKRGSRGRGRTSEEDTPKKKKHKGGSFTDTILSVHPSDVLDMPVDPNEPTYCLCHQ
 VSYGEMIGCDNPDCPIEWFHFACVDLTTKPKGK
 >BAIP2
 SQQASVTMHDVDAESFEVLVDYCYTGRVSLSEANVORLYAASDMLQLEYVREACASFLARRLDL
 CTAILKFADAFDHHKLRSQAQSYLAHNFKQLSRMGSSTREETLADLTIAQLLAIVRLLDLS
 DIESERTVCHVAVQWLEAAAKERGPSAAEVFKCVRWMHFTEDQDYLEGLLTCKIVKKYCLDVIE
 GALQMRYGDLLYKSLVPVPNSSSSSNSLVSAAENPPQRLGMCAKEMVIFFGHFRDPFLCYDPYSGD
 IYTMP SPLTSFAHTKTVTSSAVCVSPDHDIYLAQPRKDLWVYKPAQNSWQQLADRLLCREGMDV
 AYLNGYIYILGGRDPIGVKLKEVECYSVQRNQVALVAPVPHSFYFSLIVVQNYAVNSKRMLCYD
 PSHNMWLNCASLKRSDFQEACVFNDEIYCICDIPVMKVYNPARGEWRRISNIPLDSETHNYQ
 IVNHDQKL
 LLITSTTPQWKKNRVTVYEYDTREDQWINIGTMLGQFDSGFICLCAVYPSCLEPGQSFITEED
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 SHSKTRQEKRTEMYYTHEKQEKGTLNSNAAYEQSHFFNKNYTEDIFPVTPPELEETIRDEKIRRL
 KQVLREKEAALEEMRKKMHQK
 >BARD1
 LAGFESLTCSFPVVSRGLLASRSPRSLSSEGTMQDNRQPRNQPRIRSGNEPRSASAMEPDGRGA
 WAHSRAALDRLEKLLRCRCTNILREPVCGLGGCEHIFCSNCVSDCIGTGPVCYTPAWIQLDKINR
 QLDMSIQLCSKLRNLLHDNEPSDLKEDKPRKSLFNDAGNKKNSIKMWFSPRSKKVRYVVS
 KASVQTOPAIKKDASAQQDSYEVFVSPSPFADVSERAKKASARSGKKQKKTLAEINQKWNLE
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 VTPEKVCKNYILTSKKSLPLENNKGRRGHHNRLSSPISKRCRTSILSTSGDFVKQTV
 PSENIPPLECS
 SPPSCKRKVGGBTSGSKTVTCPMNSLVFHQVHLLH
 >CA150
 QQFIPGPLKILVWPCCLFQSAPTTQDQTPSSAVSVATPTVSVSTPAPTATPVQTVQPHPQTLPPA
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 KEPIKEIKEPKEEEMTEEEKAQAKPVATAPAPIPGTPWCVWTGDERVFFYNPTTRLSMWDRP
 DDLIGRADVDKIIQEPFHKKGMEELKKLRHPTPTMLSIQKWQFSMSAIKEEQLMEEINEDEPV
 KAKKR

Figure 6

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>CGI-125

FDASARNFARVSGLLLQCAGGVLVSSFVMAAAVAMETDDAGNRLRFQLELEFVQCLANPNYLNFLA
QRGYFKDKAFVNLYKQKLYWDPEYAKYLKYPQCLHMLLELQYEHFRKELVNAQCQAKFIDEQQILH
WQHYSRKRMRRLQQQALAEQQQQNNTSGK

>CGI-74

VEKARAKKREAAEVYRNSMPASSFOOKILRVCEVCSAYLGLHDNDRR~~LADEGGKL~~HLGEF~~EFREK~~
BEEFKRVAEAKQEKRNQERLKREEREREREKLRRSRSHSKNPKR

>CLH-17

MAQILPIRFQEHQLQNLGINPANIGFSTLTMSDKFICIREKVGBQAQVVIIDMNDPSNP~~IRRPI~~
SADSAIMNPASKVIALKAGKTLQIFNIEMKS~~KMKAHTMTDDVTFWKWI~~SLNTVALTDNAV~~YHWSM~~
EGESQPVKMFDRHSSLAGCQIINYRTDAKQKWL~~L~~TGISAQ~~QNRVVGAMQLYSVDRKVSQPIEGHA~~
ASFAQFKMEGNAEESTLFCFAVRGQAGGKLHII~~EVGTPPTGNQPFPKAVDVF~~FPPEAQND~~FPVAM~~
QISEKHDVVFLITKYGYI~~HL~~YDLET

>CLK1

DAWVLEHLNTTDPNSTFCVQMLEWFHHG~~H~~ICIVFELLGLSTYDFIKENGFLPFRLDH~~IRK~~MA~~Y~~
ICKSVNFLHSNKL~~T~~HTDLKPENILFVQSDY~~TEAYNPKI~~KRDERTL~~INPD~~IKVVD~~FGSATYD~~DEHHS
TLVST~~R~~HYRAPEVILALGWSQPCDVWSIGCILIEY~~YLGFTV~~FPT~~HD~~SKEH~~LAMMER~~ILG~~PLPKHMI~~
QKTRKRKYF~~H~~DR~~L~~D~~W~~DEHSSAGRYVSRRCKPL~~KE~~MLSQD~~V~~E~~H~~ERLFD~~L~~IQK~~M~~LEYDPAKRITLR
EALKH~~PPFD~~L~~KK~~SI

>DRP-1

KDNFTL~~I~~PEGVNGIEERMTVVWDKAVATGKMDENQFVAVTSTNAAKI~~F~~NL~~Y~~PRKGRIAVGSDADVV
IWDPDKLKTITAKSHKSAVEYN~~I~~FE~~G~~MECHGSPLVVISQGKIV~~F~~ED~~G~~N~~I~~NV~~N~~KGMGR~~F~~IPRKA~~F~~
HLYQRVKIRNKV~~F~~GLQGV~~S~~R~~G~~MYDGPV~~Y~~EV~~P~~AT~~P~~KYAT~~P~~APS~~A~~KSSPS~~K~~HQ~~PP~~PIRNLHQS~~N~~F~~S~~
GAQ~~I~~DDNN~~P~~R~~R~~T~~G~~H~~R~~IVAPP~~G~~GR~~S~~N~~I~~TS~~L~~G

>EF1A

MHHEALSEALPGDNVGFNVKNVS~~V~~KDVRRGNVAGDSKNDPPMEAAGFTAQVII~~I~~LN~~H~~PGQISAGY~~A~~
VLDCHTAIACKFAELKEKIDRRSGKKLEDGP~~K~~FL~~K~~S~~G~~DAAI~~V~~DMVPGKPMCVES~~F~~SDY~~P~~PLGRFA
VRDMRQTVAVGVIKAVDKKAAGAGKVT~~K~~SAQKAQKAK

>EF1G (bait)

AAGTLYT~~P~~ENWRAFKALIAAQ~~S~~GAQ~~V~~R~~V~~LSAPP~~H~~F~~H~~GQ~~T~~N~~R~~TP~~E~~FLRKF~~P~~AGK~~V~~PA~~F~~EG~~DD~~GF
CVFESNAIAYYVSNEELRG~~S~~T~~P~~AAAQ~~V~~V~~Q~~W~~V~~S~~F~~AD~~S~~DI~~V~~P~~A~~ST~~W~~V~~F~~PT~~L~~GIM~~H~~H~~N~~KQ~~A~~TEN~~A~~KE
EVRR~~I~~L~~G~~LL~~D~~AYL~~K~~TR~~T~~FLV~~G~~ER~~V~~TL~~A~~DI~~T~~V~~V~~C~~T~~L~~W~~LY~~K~~Q~~V~~LE~~P~~S~~F~~R~~Q~~A~~F~~P~~N~~T~~R~~W~~F~~L~~T~~C~~I~~N~~Q~~P~~Q~~
FRAVLGEVKLCEKMAQFD~~A~~KK~~F~~A~~E~~T~~Q~~PK~~K~~DT~~P~~R~~K~~E~~G~~S~~R~~E~~E~~KQ~~K~~P~~Q~~A~~E~~R~~K~~E~~E~~K~~K~~AA~~A~~PA~~F~~EE~~E~~EM~~D~~E
CEQ~~A~~LA~~A~~E~~P~~KA~~D~~PF~~A~~HL~~P~~K~~S~~TF~~V~~L~~E~~DEF~~K~~R~~K~~Y~~S~~N~~E~~DT~~L~~S~~V~~AL~~P~~Y~~F~~WE~~H~~FD~~K~~D~~G~~W~~S~~L~~W~~Y~~S~~Y~~R~~F~~P~~EE
LTQ~~T~~FMSCNLITG~~M~~Q~~R~~LD~~K~~LR~~K~~NA~~F~~A~~S~~V~~I~~L~~F~~GT~~N~~NS~~S~~IS~~G~~V~~W~~V~~F~~R~~G~~Q~~E~~LA~~F~~PL~~S~~PD~~W~~Q~~V~~D~~Y~~ES~~Y~~
TWRKLD~~P~~G~~S~~E~~E~~T~~Q~~TL~~V~~RE~~Y~~F~~S~~WE~~G~~A~~F~~Q~~H~~V~~G~~K~~A~~F~~N~~Q~~G~~K~~I~~F~~K~~

>EF1G (prey)

AAGTLYT~~P~~ENWRAFKALIAAQ~~S~~GAQ~~V~~R~~V~~LSAPP~~H~~F~~H~~GQ~~T~~N~~R~~TP~~E~~FLRKF~~P~~AGK~~V~~PA~~F~~EG~~DD~~GF
CVFESNAIAYYVSNEELRG~~S~~T~~P~~AAAQ~~V~~V~~Q~~W~~V~~S~~F~~AD~~S~~DI~~V~~P~~A~~ST~~W~~V~~F~~PT~~L~~GIM~~H~~H~~N~~KQ~~A~~TEN~~A~~KE
EVRR~~I~~L~~G~~LL~~D~~AYL~~K~~TR~~T~~FLV~~G~~ER~~V~~TL~~A~~DI~~T~~V~~V~~C~~T~~L~~W~~LY~~K~~Q~~V~~LE~~P~~S~~F~~R~~Q~~A~~F~~P~~N~~T~~R~~W~~F~~L~~T~~C~~I~~N~~Q~~P~~Q~~
FRAVLGEVKLCEKMAQFD~~A~~KK~~F~~A~~E~~T~~Q~~PK~~K~~DT~~P~~R~~K~~E~~G~~S~~R~~E~~E~~KQ~~K~~P~~Q~~A~~E~~R~~K~~E~~E~~K~~K~~AA~~A~~PA~~F~~EE~~E~~EM~~D~~E
CEQ~~A~~LA~~A~~E~~P~~KA~~D~~PF~~A~~HL~~P~~K~~S~~TF~~V~~L~~E~~DEF~~K~~R~~K~~Y~~S~~N~~E~~DT~~L~~S~~V~~AL~~P~~Y~~F~~WE~~H~~FD~~K~~D~~G~~W~~S~~L~~W~~Y~~S~~Y~~R~~F~~P~~EE
LTQ~~T~~FMSCNLITG~~M~~Q~~R~~LD~~K~~LR~~K~~NA~~F~~A~~S~~V~~I~~L~~F~~GT~~N~~NS~~S~~IS~~G~~V~~W~~V~~F~~R~~G~~Q~~E~~LA~~F~~PL~~S~~PD~~W~~Q~~V~~D~~Y~~ES~~Y~~
TWRKLD~~P~~G~~S~~E~~E~~T~~Q~~TL~~V~~RE~~Y~~F~~S~~WE~~G~~A~~F~~Q~~H~~V~~G~~K~~A~~F~~N~~Q~~G~~K~~I~~F~~K~~

>FEZ1

GNCSIDTEIHEKEEEEFNEKSENDSGINEEPLLTADQVIEEIEEMM~~Q~~NSPDPEEEEVLEEDG~~G~~GET
SSQADSVL~~Q~~EMQALTQ~~T~~FNNNWSYEG~~L~~R~~H~~MSG~~S~~ELTE~~L~~D~~Q~~VEGA~~I~~R~~D~~F~~S~~E~~E~~LV~~Q~~QL~~A~~R~~D~~E~~E~~LF
EKEVKNS~~F~~ITV~~L~~I~~E~~V~~Q~~NK~~Q~~KE~~Q~~REL~~M~~K~~K~~R~~K~~E~~G~~LS~~L~~Q~~S~~R~~I~~E~~K~~G~~N~~Q~~M~~PL~~K~~R~~F~~S~~M~~E~~G~~I~~S~~N~~I~~L~~Q~~SG~~I~~
RQTFGSSGTD~~K~~Q~~Y~~L~~N~~T~~V~~I~~P~~YEKKAS~~P~~PS~~V~~ED~~L~~Q~~M~~I~~T~~N~~I~~L~~F~~AM~~K~~ED~~N~~E~~K~~V~~P~~TL~~L~~T~~D~~Y~~I~~L~~K~~V~~L~~C~~P~~T

Figure 6 (continued)

>G45IP1
 MASSGGELGSLFDDHHVQRAVCDTRAKYREGRRPRAVKVYTINLESQYLLIQGVPAVGVMKELVERF
 ALYGAIEQYNALDEYPAEDFTEVYLIKFMNLQSARTAKRMDEQSFFGGLLHVCYAPEFETVEETR
 KKLQMRKAYVVKTTENKDHYVTKKKLVTEHKDTEDFRQDFHSEMSGFCKAALNTSAGNSNPYLPYS
 CELPLCYFSSKCMCSSLGGPVDRAPDSSKDGRNHKTGMGHYNHNDSLRKTQINSLKNSVACPGIAQKA
 ITSSEAVDRFMPRTTOLQERKRRREDDRKLGTFLOTNPTGNEIMIGPLPDISKYDMHDDSI_NTTA
 NITRKHLKEVTSVPKPPEDKPEDVHTSHPLKQRRRI

>G45IP2
 RTCMPYIFSLSLEALKCFRIRNNEKMLSDSHGVETIRDILPDTSLGGPSFFKIITAKAVLKLQAGN
 AEEAALWRDLVVKVLASYLETAAEAVLGGSLDENQEVLFATRENGFLQYLVIAIPMEKGQLDSQ
 GCFCAAGCSRQIGFSFVRPKLCAFSGLYYCDICHQDDASVIRARIHWNWLTKRPICRQALKFLTQI
 RAQPLINLQMVNASLYEHVERMHILIGRRREQLKLLGDYLGLCRSGALKELSKRLINHRNYLESPHR
 FSVADLQQIADGVYEGFLKALIEFASQHVVHCDLCTQRGFICQICQHHDIIFPFEEFTTVRCAECK
 TVFHQSCQAVVKKGCPRCARRRKYQEONIFA

>G45IP3
 PNRGPLSPPNDLRPSHVISLPLHNAPHTRPTNQHTNHIPMMARCNTRKHIPRPPHTCPKRP5IRD
 NPIYYLRSFFLRRIFLSLLPLQPSYPPIRRALAPNRHHPAKSPRSPTPKHIRITRIRSINHLSSP
 >GADD45G
 GAGAEGGLECGWSWGAKGVCRWPGGLSPRPPAGSRSLRWLLRRMQGAGKALHELLLSAQROGCLT
 AGVYESAKVLMVDPDNVTFCVLAAGEEDEGDIALQIHFTLIQAFCCENDIDIVRVGDVQRLAAIVG
 AGEEAGAPGDLHICILISNPNEADWKDPALEKLSLFCEESRSVNDWVPSITLPE

>GIJ1
 PQMADRSRQKCMQSLLSELAKAAKKLQALSNRLFEELAMDVYDEVDRRENDAVWLATQNHS
 VTERSAVPFLPVNPEYSATRNQGRQKLARFNAREFATLIIDILSEAKRRQQGKSLSSPTDNLELSL
 RSQSDDQHDDQHDSVASDEDTDQEPLRSTGATRSNRARSMDSSDLSDGAVTLQEYLELKKALATSE
 AKVQLMKVNSSLSDELRRLQREIHKLQAEENLQLRQPPGPVPTPLPSERAHTPMAFGG9THRRD
 RQAFSMYEPGSALKPFGGPPGDELTTRLQPFHSTELEDDAIYSHVHPAGLYRIRKGVSASAVPFTP
 SSPLLSCSQEGRHTSKLSRHGSADSDYENTQSGDPLLGLEGKRFLELGKEEDFHPELESLDGDL
 DPGLPSTEDVILKTEQVTKNIQELLRAAQUEFKHDSFVPCSEKIHLAVTEMASLFPKRPALEPVRSS
 LRLLNASAYRLQSECRKIVPPEPGAPVDFQLLTQQVIQAYDIAKAAKQLVTITREKKQ

>hADA3
 KDVDALLKKSEAQHEQPEDGCPFGALTQRLLQALVEENIISPMEDSPIPDMSGKESGADGAS TSPR
 NQNKPFSPHTKSLESRIKEELIAQGLLESDRPAEDSEDEVLAELRKRQAEALKALSAHNRTKKHD
 LLRLAKEEVSRQELRQVRMADNEVMDAFRKIMAARQKKRTPTKKEKDQAWKTLKERESILKLLDG

>HB01
 DAERQEAALGIVRRIGTDTEAATEPAGATVPAAAAARIGTVGPQPPAMPRRKRNAGSSSDGTEDSD
 FSTDLEHTDSSESDGTSSRSARVTRSSARLSQSSQDSSPVRNLQSFTEPAYSTRVTRSQQQOPT
 PVTPKYPLRQTRSSGSETEQVVDFSDRETKNTADHDESPPTPTGNAPSSESIDIDISSPNVSHDE
 SIAKOMSLKDSGSDLSHRPKRRRFHESYNFNMKCPTPGCNSLGHLTGKHERHFSISGCPLYHNLSA
 DECKVRAQSRDKQIEERMLSHRQDDNNRHATRHQAPTERQLRYKEVAAELKKRNGLSKEQKEKY
 MEHRQTYGNTREPLLENLTSEYDLDLFRRQARASEDLEKLRILQGQITEGSNMIKTIAGFRYELDT
 WYHSPYPEEYARLGRLYMCEFCLKYMKSQTLRRHMAKCVWKHPPGDEIYRKGSISVFEVDGKKNK
 IYCQNLCLLAKLFLDHKTLYYDVEPFLFYVMTEADNTGCHLIGYFSKEKNSFLNVNVSCILTMPQY
 MRQGYGKMLIDFSYLLSKVEEKVGSPERPLSDLGLISYRSYWKEVLLRYLHNFGKEISIKEISQE
 TAVNPVDIVSTLQALQMLKYWKKGKHLVLKRODLIDEWIKEAKRSNSNKTMDPSCLKWTTPKG

Figure 6 (continued)

>HD1.7

MATLEKT

PQPPPPPPPPPPGPVAEELPLRPKKELSATKKDRVNHCLTICENIVAQSVRNSPEFQKLLGIAME
LFLLCSDDAESDVRMVADECLNKVIKALMDSNL-PRLQLÉLYKEIKKNGAPRSILRAALWRFAELAHL
VRPQKCRPYLVNLLPCLRTSKRPEESVQETLAAAVPKIMASFGNFANDNEIKVLLKAFIANLKSS
SPTIRRTAAGSAVSICQHSRRTQYFYSWLLNVLLGLLVPVEDEHSTLLTGVLVLLTSR
>HDD1.3

PRLOLELT

AAVPKIMASFGNFANDNEIKVLLKAFIANLKSSPTIRRTAAGSAVSICQHSRTQFYSWLLNVL
LGLLVPVEDEHSTLLILGVLLTLRYLVPLLQQQVKDTSLKGSFGVTRKEMEVPSAEQLVQVYELT
LHHTQHQDHNVVTGALELLQQLFRTPPPELLQTLTAVGGIGQLTAKEE5GGRSRSGSIVELIAGG
GSSCSPVLSRKQKGKVLGEEEFALEDDSESRSVDSSALTASVKDEISGELAASSGVSTPGSAGHD
IITEQPRSQHTAGGLSGSGQL

>HDexQ2 0

>HDex051

ADDITION

ADIBQGHDRKRFMEQFTKLKDLFYRSSNLQYFKRLIQIPQLPENPPNFLRASALSEHISPVVVIAE
ASSPDSEPVLEKDDLMMDMASQQLNFDNKFDDIFGSSFS9DPFNENSONGVNKDEKDHLIERLYRE
ISGLKAQLENMKTESQRVVLQLKGHVSELEADLAEQQHLRQQAADDCEFLRAELDELRRQREDTEK
AQRSLSIERKAQANEQRYSKLKEKYSELVQNHADLLRKNAEVTQVSMARQAQVDLEREKKELED
SLERISDQGQRKTQELEVLESLKQELATSORELQVLOGSLETSAQSEANWAAEFÄELEKERDSL
SGAAHREEELSALRKELODTQLKLASTEESMCQLAKDQRKMLLVGSRKAAEVOIODOASTRP
>HIP11

VIDI VTA

DEVIADIRICAQDAFFQVKEVDVGLAADVGTIQLPKVIGNQSLVNELAFTARKMMADEALGSG
LVSRRVFPDKEVMILDAALALAAEISSKSPVAVQSTKVNLLYSRDHSAESLNVVASWNMSMLQTQDL
VKSVQATTENKELKTVTFSKL

SHIP13
PASSED

PCCSEDTIPSQVSDYDFSVSGDQEADQQEFDKSSTIPRNSDISQSYRRMFQAKRPASTAGLPTTL
GPAMVTPGVATIRRTPSTKPSVRRGTIGAGPIPIKTPVPIVKTPTVPDLPGVLPAPPDGPEERGEH
SPESPSPVGEGPQGVTSMPSSMWSGQASVNPLPGPKPSIPEEHHQAIPESEAEDQEREPPSATVSP
GQIPESDPADLSPRDTPOGEDMLNAIRRGVILKKTTTNDRSAPRS
>H1P15

1115
THURSDAY

ITIAPPNLNMIETFICQVCEETLAHSVDSLEQLTGIRMLRHLTMTIDYHTLIANYMSGFLSLLT
TANARTKFHVLMILLNLSENPAVAKKLFSAKALSIFVGLFNIETNDNIQIVIKMFQNIISNIIKSG
KMSLIDDDFSLEPLISAFREFEELAKQLQAQIDNQNDPEVGQOS.

Figure 6 (continued)

>HIP16

DEEERNHRQMIKEAFAGDDVIRDFLKEKREAVEASKPKDVLTLPGWGEWGGVGLKPSAKKRRRFL
 IKAPEGPPRDKNLNPVIIINEKRNIHAAAHQVRVLPPFTTHWQFERTIQTPIGSTWNTQRAFQKL
 TTPKVVTKPGHIINPIKAEDVGYRSSSRDLSVIQRNPKRITTRHKKQLKKCSVD

>HIP2

MANIAVQRIKREFKEVLKSEETSKNQIKVDLVDENFTELRGEIAGPPDTPYEGGRYQLEIKIPETY
 EPPEDPKARFETKIMWBNISSVIGAICEDTLEKDWAAAMTIRTULLSLOALIAAEPDDPQDAVAN
 QYKQNPEMFKOTARLWAHIVYAGAPVSSPEYTKKIELCAMGFDRNAVIVALSSKSWDVTATELL
 SNX

>HIP5 (bait)

FLKSLILKESKYEHGYLKALIINQSFKFGNQKAAAIRDSIELTKEKGAEIPKTIKKLRWFDETSNI
 ENNAENSHSLKNKTGTTQQHSQQFHIQSGAGSNIIISVSTCAVNSADTKKSREDSISENVTTLGGSG
 ADHMPNCFIPSGYNFAKHAWPASKKEESKIPVHDDSKTKQGKQRGRAKIIRKPGSAKVQSGFIC
 TNRKGAVIQPQASAKVNIFTQAQGKLIIPCPQQSTSNIIRSGKNIQVSQCPVTPENPONIITHNS
 FNSKHVLPTEHSLNQWNQESSSPLSNACSDLVTVPISLPSYCSECQTFAKINHSNGTQAVARQDA
 TLYCTQRSPVCEESYPSVTLRTAEEESVPLWKRGPNVLHQNKATGSTMRRKRIAETKRRNILEQ
 KRQNPQSGVGQKYSEQINNFGQSVLLSSSEPQTTTRGTSYIEEVSDSTSEFLMAENLVKASVPEDEI
 LTVLNSKQIQLQSNLPLNKTQOFNICTLSAEEQKILESLNDLNERLHYIQESICKNPSIKNTLQIIP
 LLEKREDRTSSCRDKR

>HIP5 (prey)

FLKSLILKESKYEHGYLKALIINQSFKFGNQKAAAIRDSIELTKEKGAEIPKTIKKLRWFDETSNI
 ENNAENSHSLKNKTGTTQQHSQQFHIQSGAGSNIIISVSTCAVNSADTKKSREDSISENVTTLGGSG
 ADHMPNCFIPSGYNFAKHAWPASKKEESKIPVHDDSKTKQGKQRGRAKIIRKPGSAKVQSGFIC
 TNRKGAVIQPQASAKVNIFTQAQGKLIIPCPQQSTSNIIRSGKNIQVSQCPVTPENPONIITHNS
 FNSKHVLPTEHSLNQWNQESSSPLSNACSDLVTVPISLPSYCSECQTFAKINHSNGTQAVARQDA
 TLYCTQRSPVCEESYPSVTLRTAEEESVPLWKRGPNVLHQNKATGSTMRRKRIAETKRRNILEQ
 KRQNPQSGVGQKYSEQINNFGQSVLLSSSEPQTTTRGTSYIEEVSDSTSEFLMAENLVKASVPEDEI
 LTVLNSKQIQLQSNLPLNKTQOFNICTLSAEEQKILESLNDLNERLHYIQESICKNPSIKNTLQIIP
 LLEKREDRTSSCRDKR

>HMP

QBQVKIESLAKSLEDALRQTASVTLQAIAAQNAAVQAVNAHSNILKAAMDNSEIAGEKKSAQWRTV
 EGALKERRKAVDEAADALLKAKEELEKMKSVIENAKKKEVAGAKPHITAAEGKLHNMIVDLDNVK
 KVQAAQSEAKVVSQYHELVVQARDDFKRELDSTPVEVLPGWKGMSVSDLADKLSTDDLNSLIAH
 RRIDQLNRELAEQKATEKOHITLALEKQKLEEKRAFDASAVALAKALEHHRSEIQAEDRKIEEVRDAM
 ENEMRTQLRROAAHTDHLRDVLRVQEQLSEFQNLSEQELQFRRRLSQEQVDNFTLDINT
 AYARLRGIEQAVQSHAVAEEEARKAHQLWLVEALKYSMKTSSAETPTIPLGSAVEAIKANCSDNE
 FTQALTAIIPPESLTRGVYSEETLRARFYAVQKLARRVAMIDETRNSLYQYFLSYLQSLLLFPQO
 LKPPPELCPEDINTFKLISYASCYIEHGDILELAAKFVNOLKGESRRVAQDWLKEARMTLETQIIVE
 ILTAYASAVGIGITQVQPE

>HP28

PPADSLIJKYDTPVLVSRNTEKRSPKARLLKVSQQPGPSGSAPQPPKTKLPSTPCVPDPTKQAEII
 LNAILPPREWVETQLWIQQVSSTPSTRMDVVHLQEQQLDLKLQQRQARETGICPVRRELYSQCFDE
 LIREVTINCAERGLLLLRLRDEIRMTIAAYQTLYESSVAFGMRKALQAEQGKSDMERKIAELETEK
 RDLERQVNEQKAKCEATEKRESERRQVEEKKHNEEIQFLKRTNQQLKAQLEGI IAPKK

>HSPC232

ERRADGCIYGVSRARVAYRDEMSEGRYERYI PRERAPPRSHPSDESGYRWRDDHSASRQP
 EYRDMRDGFRRKSFYSSHYARERSPYKRDNTFFRESPVGRKDSPHSRGSSVSSRSYSPERSKSYS
 FHQSQHRNKERPVQSLKTSRDTSPSSSGSAVSSSKVLDKPRLTEKELEAAASKWAAEKLEKSDESN
 LPHISEYEAGSTAPLFTDQPEEPESNTTHGIELFEDSQLTTRSKAIASKTKEIEQVYRQDCETFGM
 VVKMLIEKDPSLEKSIQFALRQNLHEIGERCVEELKHFIAEYDTSTQDFGEFF

Figure 6 (continued)

>HYPA

GRRRSSLSPTMRPGTGAERGGIMMGHPGMHYAPGMHPMGQRANMPPVPHGMPQMMPPMGGPPMG
 QMPGMMSVMPGMMMSHMSQASMQPALPPGVNSMDVAAGTASGAKSMWTEHKSPDGRRTYYNTETK
 QSTWEKPDDLKTPAEQLSKCPWKEYKSD9GKPYYNSQTKESRWAKPKELEDLEGYQNTIVAGSL
 ITKSMLHAMIKAEESSKQFECTTSTAPVPTTEIPTTMSTMAAAEAAAAVVAAAAAAAANA
 NASTSASNTVSGTVPVVEPEVTSIVATVVDNENTYTISTEEQALTSRAIODOSSVVSQNEGBH
 TSQETVADFTPKEEEEESQAKTWTNTKEEAKQAFKELIKEKRVPSNASWEQAMKMIINDPRY
 SALAKLSEKKQAFNAYKVQAKKEKKKKKK

>HZFH

HARFAAECLAESHQHLSKESLAGNKPANAVLHKVILQLEELLSDMKADVTRLPATLSRIPPIAAR
 LQMSERSILSRLASKGTPEHPTPAYPPGPYATPPGYGAFAFSAPVGALAAAGANYSQMPAGSFITA
 ATNGPPVLVKEKEKEMVGALVSDGLDRKEPRAGEVICIDD

>IKAP

LKEGSPLEDLALLEALSEVVQNTENLKDEVYHILKVLFLFEFDEQGRELQKAFEDTLQLMERSLPE
 IWTLTYQONSATPVLGPNSTANSIMASYQQQKTSVPVLDALFIPPKINRRRTQWKLSLDD

>IMPD2

DFLILPGYIDFTADQVDLTSALTKKITLKTPLVSSPMĐTVEAGMAIAMALTGGIGFIHHNCTPEF
 QANEVRKVKKYEQGFIIDPVVLSPKDRVRDVFEAKARHGFCGIPITDTGRMGSRLVGIISSRDIDF
 LKEEEHDCFLEIMTKREDLWVAPAGITLKEANEILQRSKKGKLPIVNEDDELVAI IARTDLKKNR
 DYPLASKDAKKQLLCGAAIGTHEDDKYRLDLLAQAGVDVVVLDSQGNSIFQINMIKYIKDKYPNL
 QVIGGNVVTAAQAKNLIDAGVDALRVMGSGSICITQEVLACGRPQATAVYKVSEYARRFGVPVIA
 DGGIQNVGHIAKALALGASTVMMGSLLAATTEAPGEYFFSDGIRLKKGYRGMGLDAMDKHLSSQNR
 YFSEADKIKVQGVSGAVQDKGSIHKFVPLIAGIQHSCQDIGAKSLTQVRAMMYSGELKEKRTS
 SAQVEGGVHSLHSYEKRLF

>KPNA2

AWALTNIASGTSEQTKAVVDGGAIPAFISLLASPHAHISEQAVWALGNILAGDGSVFRDLVIKYGAV
 DPLLALLAVPDMSLACGYLRNLTWTLNSNLCRNKNPAPPIDAVEQILPTLVRLLHHDDPEVLA
 WAIISYLTDPGPNERIGMVVKITGVVPQLVKLLGASELPIVTALRAIGNIVTGTDEQTQVVIDAGALA
 VFPSSLTNPKTNIQKEATWTMSNITAGRQDQIQQQVNVHGLVPFLVSLSKADFKTQKEAVWAINTY
 TSGGTVEQIVYLVHCGITEPLMNLLIAKDTKIIILVILDAISNIFQAAEKLGETEKLSSIMIEECGGL
 DKIEALQNHENESVYKASLSLIEKYFSVEEEEEDQNVVPETTSEGYTFQVQDGAPGTFNF

>KPNB1

LAAGVLVGDLCRALQSNITIPFCDEVMQLLLENLGNEVHRSVVKPQILSVFGDIALAIGGEFKKYLE
 VVLNTLQQASQAQVDKSDYDMVDYLNELRESCLEAYTGIVQGLKGDOENVHPDVMLVQPRVEFILS
 FIDHIAGDEDHTDGVVACAAGLIGDLCTAFGKDVLKLVEARPMIHELLTEGRRSKTNKAKTLATWA
 TKELRKLKNQA

>Ku70

KTRTFNTSTGGLLLPSDTKRSQIYGSRQIILEKEETEELKRFDDPGILMGMFKPLVLLKKHYLRP
 SLFVYYPEESLVIQSSTLFSALLIKCLEKEVAALCRYTPRRNIPPYFVALVPQEEELDDQKIQVT
 GFQLVFLPFADDKRKMPFTEKIMATPEQVGKMKAIIVEKLRFTYRSDSFENPVLQHQFRNLEALALD
 LMEPEQAVDLTPKVEAMNKRGLGSVDEFKELVYPPDYNPEGKVTKRKHDNEGSGSKRPKVEYSEE
 ELKTHISKGTLGKFTVPMLEACRAYGLKSGLKKQELLEALTKHQD

>LUC7B1

VDAAVDAAAASAKAEKVHELNEKIGKLLAKAEQLGAEGNVDESQKILMEVEKVRACKKEAEEYR
 NSMPASSFOQQQKLRVCEVCSAYLGLHDNDRRLADHFGKLHLGFIQIREKLDQLRKTVAEKQEKR
 QDRLRRREEREREERLSRRSGSRTRDRRRRSRSRSTSRERRKLSRSRSRDRHRRHRSRS
 RSHSRGHRRASRDRSAKYKFSRERASREESWESGRSERGPPDWRLESSNGKMAARRSEEKEAGEI

Figure 6 (continued)

>MAGEH1
ÄSFPTAVSFEPPLAGDMPRGRKSRRRNARAAEENRNNRKIQASEASETPMAASVVASTPEDDLG
PEEDPSTPEEASTTPEEASSTAQAQKPSVPRSNFQGTTKSSLMSILALIFIMGNSAKEALVWKVLG
KLGMQPGRQHSTIFGDPKKIVTEEFVRRGILYKPVPRSSPVEYEFFWGPRAHVESSKLKVMHFVAR
VRNRCSKDWPCNYDWDSDDAEVEAILNSGARGYSAP
>MAP11c3
QRRSFADRKKEVQGTRDQHPSKIPVIIERYKGEKOLPVLDKTKFLVDPDHVNMSELVKIIRRRLQLN
PTQAFFLLVNQHSMVSVSTPIADIYEQEKDEDGFLYMYASQETFGF
>mHAP1
PKEQVQSGAGDGTGSGDPAAGTPPTQAVGPAPEPSAEPKPAPAQGTGSGQKSGSRKTGSCFCRSM
IIGDSDAPWTRYVFQGPYGRATGLGTGKAEGIWKTPAAYIGRRPGVSGPERAAFIRELQEAICPN
PPPTKKITEDDVKVMLYLLEEKERDLNTAARIGQSLVKQNSVLMEEINNLETMLGSAREEILHLRK
QVNLRDDLLQLYSDSDDDDDEEDEEDEEEGEEEEEQGRDQDQHQDHPYGAQPKPHPKAETAHRCPQ
LETLQQKLRLLLEEENDHLCREEASHLDNLEDEEQMLILECVEQFSEASQMAELSEVVLVRLEGYR
QQKEITQLOQAEITKLQQRQCQSYGAQTEKLQQLASEKGIRHESILRAGSYMODYGSRPRDRQEDGKS
HRQRSSMPAGSVTHYGSVPDALPSFETLAEELRTSLRKFITDPAYFMRDTHCREGRKKEQR
AMPPPPAX
>mp53
VTETPGVAPAPATPWPLSSFVPSQKTYQGNYGFHLGFLQSGTAKSVMCTYSPPINLFCQLAKTC
FVQLWVSATPPAGSRVRAMAIYKKSQHMTEVVRCPHHERCSDGDGLAPPQHLLRVEGNLYPEYLE
DRQTFRHSSVVVPYEPPEAGSEYTTIHYKMCNSSCMGGMNRRIPILTITILEDSSGNLLGRDSFVR
VCACPGDRRTEEEFRKKEVLCPELPPGSAKRALPTCTSASPPQKKPLDGEYFTLKIRGRKRFE
MFRELINEALELKDAHATEESGDSRAHSSYLTKKGQSTSRRHKKTMVKVGPDS
>NAG4
RDRVENEAEKDLQCHAPVRLDLPPEKPLTSSLAKQEEVEQTPLQEAALNQLMROLQRKDPSAFFSFP
VTDFIAPGYSMIIKHPMDSTMKEKIKNNDYQSIEELKDNFKLMCTNAMITYNKPETIYYKAACKLL
HSGMKILSQERIQLQKQSIDFMADLQKTRKQKDGTDSQSGEDGGCWQREREDSGDAEAHAFKSPS
KENKKDKDMLEDKFKSNNLEREQEQQLDRIVKESGGKLTTRRLVNSQCEFERRKPDGTTLGLHPV
DPIVGEPGYCPVRLGMMTGTQLQGVNTLQGFKEDKRNKVTPLVLYNYGPYSSYAPHYDSTFANISK
DDSDLIYSTYGEDSDLPSDFSIEFLATCQDYPYVMADSLLDVLTKGHSRTLQEMEMSLPEDEGH
TRTLDTAKEMEITEVEPPGRILDSSTQDRLIALKAVTNFGVPVEVFDSEEEAIQKLLDETRLLRE
LQEAQNERLSTRPPPNCILLGPSYREMHLAEQVTNNLKELAQQTFTGDIVSTYGVRKAMGISIPS
PVMMENNFVDLTEDTEEPKKTDAECGPCCS
>NEFL
LSPLSSLSGLPPPPRAGEPPAATMSSFSYEPYYSYKRRYVETPRVHISSVRSGYSTARSAYSSY
SAPVSSSLSVRSYSSSSGSLMPSLENLDLSQVAASNDLKSIRTQEKALQDNLDRFASFIERVH
ELEQQNKVLEAELLVLRQKHSEPSRFRALYEQEIRDLRLAAEDATNEKQALQGEREGLEETLRNLQ
ARYEEEVLSREDAEGRIMEARKGADEAALARAELEKRIDSIMDEISFLKKVHEEEIAELQAAQIQA
QISVEMDVTKPDLSAALKDIRAQYEKLAAKNMQNAEEWFKSRTFTLTESAKNTDAVRAAKDEVSE
BRLLLKAKTLEIEACRGMNEALEKQLQELEDKQNADISAMQDTINKLENELRTKSEMARYLKEYQ
DLLNVKMAVDIEIAAYRKLEGEETRLSFTSVGSITSGYSQSSQVFGRSAYGLQTSSYLMSTRSF
PSYYTSHVQEEQIEVEETIEAAKAEAKDEPPSEGEAEEEEKDEEEAEEEEAAKEESEEA
KEEEEGGEGEGEETKEAEEEKKVEGAGEEQAACKKD
>p53
MEEPQSDPSVEPLSQETFSDLWKLIPENNVLSPLSQAMDDMLSPDDIEQWFTEDPGPDEAPRM
PEAAPPVAPAPAAPTPAAPAPAPSWPLSSVPSQKTYQGSGYFRLGFLHSGTAKSVTCTYSPALNK
MFCQLAKTCVPQLWVDSTPPGTRVRAMAIYKQSQHMTEVVRCPHHERCSDSDGLAPPQHLLRVE
CNLRVEYLLDRNTFRHSVVVPYEPPEVGSDCTTIIHYNMCMNSSCMGGMNRRIPILTITILEDSSGNL
LGRNSFVRVCACPGDRRTEEEENLRKKGEPHELPPGSTKRALPNNTSSPQPKKKPLDGEYFTL
QIRGRERFEMFRELINEALELKDAQAGKEPGGSRAHSSHLKSKKQSTSRRHKKLMFKTEGPDS

Figure 6 (continued)

>PFN2
 APRRPRCSAKGSKMAGWQSYVDNLMCDGCCQEAIIVGYCDAKYVWAATAGGVFQSITPIEIDMIVG
 KDRGFFTNGLTLGAKKCSVIRDSLVDGDCMDIRTKSQGGEPTYNVAVGRAGRVLVFVMGKEGV
 HGGGLNKKAYSMAKYLRDSGF
 >PIASy (bait)
 LVEAKNMVMSFRVSDLQMLLGFGVGRSKSGLKHELVTRALQVQFDCSPELFKKIKELEYETRYAKN
 SEPAQPHRPLDPLTMHSTYDRAGAVPRTPLAGPNIDYPVLYGKYLNGLGRPAKTLKPEVRLVKL
 PFFNMLDELLKPTELVQNNEKLQESP C I F A L T P R Q V E L I R N S R E L Q P G V K A V Q V V L R I C Y S D T S C
 P Q E D Q Y P P N I A V K V N H S Y C S V P G Y Y P S N K P G V E P K R P C R P I N L T H L M Y L S S A T N R I T V T W G N Y G K S
 Y S V A L Y L V R Q L T S S E L L Q R L K T I G V K H P E L C K A L V K E K L R L D P D S E I A T T G V R V S L I C P L V K M R L S
 V P C R A E T C A H L Q C F D A V F Y L Q M N E K K P T W M C P V C D K P A P Y D Q L I I D G L L S K I L S E C E D A D E I E Y L V
 D G S W C P I R A E K E R S C S P Q G A I L V L G P S D A N G L L P A P S V N G S G A L G S T G G G P V G S M E N G K P G A D V V
 D L T L D S S S S E D E E E E E E D E D E E G P R P K R R C P F Q K G L V P A C
 >PIASy (prey)
 LVEAKNMVMSFRVSDLQMLLGFGVGRSKSGLKHELVTRALQVQFDCSPELFKKIKELEYETRYAKN
 SEPAQPHRPLDPLTMHSTYDRAGAVPRTPLAGPNIDYPVLYGKYLNGLGRPAKTLKPEVRLVKL
 PFFNMLDELLKPTELVQNNEKLQESP C I F A L T P R Q V E L I R N S R E L Q P G V K A V Q V V L R I C Y S D T S C
 P Q E D Q Y P P N I A V K V N H S Y C S V P G Y Y P S N K P G V E P K R P C R P I N L T H L M Y L S S A T N R I T V T W G N Y G K S
 Y S V A L Y L V R Q L T S S E L L Q R L K T I G V K H P E L C K A L V K E K L R L D P D S E I A T T G V R V S L I C P L V K M R L S
 V P C R A E T C A H L Q C F D A V F Y L Q M N E K K P T W M C P V C D K P A P Y D Q L I I D G L L S K I L S E C E D A D E I E Y L V
 D G S W C P I R A E K E R S C S P Q G A I L V L G P S D A N G L L P A P S V N G S G A L G S T G G G P V G S M E N G K P G A D V V
 D L T L D S S S S E D E E E E E E D E D E E G P R P K R R C P F Q K G L V P A C
 >PLIP
 GEIIEGCRLPVLRNQDNEDEWPLAEILSVKDISGRKLFYVHYIDFNKRLDEWVTHELDLKKIQF
 PKKEAKTPKNGLPGSRPGSPEREVKRKVEVVSPATPVPSETAPASVFPQNGAARRAVAAQPGRKR
 KSNCLGTDQSQDSSDGIAPSAPMTGSLVSDRSHDDIVTRMKNIECIELGRHRLKPWYFSPYPQEL
 TTLPVLYLCEFCLKYGRSLKCLQRHLTKCDLRHPPGNEIYRKGTISFFEIDGRKNKSYSQNLCLLA
 KCFLDHKTLYYDTDPFLFYVMTEYDCKGFHIVGYFSKEKESTEDYNVACILTLPFYQRRGYGKLLI
 EFSYELSKVEGKTGTPEKPLSDLGLLSYRSYWSQITLEILMGLKSESGERPQITINEISEITSIKK
 EDVISTLQYLNLLINYYKGQVILTLSEDIVDGHERAMLKRLRIDSKCLHFTPDKWSKRGKW
 >PTN
 LSQRQDQVPRLPVQKSROESPRAEENPKWREGKKETSESSVQKAGRAAAQAGAAASRVPGLSGSN
 LAPCNKGRLSAREDVSNSKMQAQYQQQRRKFAAAFLAFIFI LAAVDTAEAGKKEKPEKKVKKSDC
 GEWQWSVCVPTSGDCGILTREGITRTGAECIKQTMKTQRCKIPCNWKKQFGAECKYQFQAWGECDLNT
 ALKTRTGSILKRALHNAECQKTVTJSKPCGKLT KPKPQAEKKKKKEGKKQEKMLD
 >PTPK
 SNYINAALMDSYRQPAAFIVTQYPLPNTVKDFWRLVYDYGCTSIVMLNEVDLSQGCPQYWPEEGML
 RYCGPIQECMCSMDCDVINRIFRICNLTRPQEGYLMVQQFOYLGWASHREVPGSKRSFLKLILQV
 EKWQECEEGEGRTIHCLNGGGRSGMFCAIGIVVEMVKRQNVDVFHAVKTLRNSKPNMVEAPEQ
 YRFCYDVALEYLESS
 >SETBD1
 KASTSGLGKDEGDIKQAKKEDTDRNKMSSVTESSRNYGYNPSPVKPEGLRRPPSKTSMHQSRL
 MASAQSNPDDVLTLSSTSESEGESGTSRKPTAGQTSATAVDSDDIQTISSGSEGDDFEDKKNMGTGP
 MKRQVAVKSTRGFALKSTHGIAIKSTNMASVDKGESAPVRKNTRQFYDGEESCYIIDAKLEGNLGR
 YLNHSCSPNLFVQNVFVDTHDLRFPWVAFFASKRIRAGTELWDYNYEVGSVEGKELLCCGAIEC
 RGRLL

Figure 6 (continued)

>SH3 GL3

VÄGLKKQFHKÄSÖLFSEKISGAEGTKLDDEFLDMERKIDVINKVVAEILSKTEYLQPNPÄYRAKL
 GMLNTVSKIRGQVTTGYPQTEGILLGDCMLKYGKELGEDSTFGNALIEVGESMKLMAEVKDSDLIN
 VKÖTFIDPLQLLQDKDLKEIGHHLKKLEGGRÄLDYKKRVCKİPDEEVROAVEKFEESKELAERS
 MFNFLENDVEQVSQLAVFIEAALDYHRQSTEILQELQSKLOMRSAAASVPRREYKPRPVKRSSSE
~~ENGVSTTSEVETTCGNSIPMDQRCRGSLVDEPENQCHLCPKCDLITLITQEDENWYEGMHEHESG~~
 FFPINYVEVIVPLPQ

>SUMÖ-2

RPRÄQLRRESGGAESVTRPLRAASAPPRAARAAMSEEKPKEGVKTENDHINLKVÄGQDGSVVQF
 KIKRHTPLSKLMKAYCERQGLSMRQIRFRFDGQPINETDTPAQLEMEDEDTIDVFQQQTGGVPESS
 LAGHSF

>SUMÖ-3

PSSTAAÄSPFCRSWCCLCAREVRTWYLFCEAAAEETPALAMADEKPKEGVKTENNDHINLKVÄGQD
 GSVVFKIKRHTPLSKLMKAYCERQGLSMRQIRFRFDGQPINETDTPAQLEMEDEDTIDVFQQQTG
 GVV

>TALL

SSPVKRQRMESALDQLQFTTVVADTGDFHAIDEYKPQDATTNPSLILAAAQMPAYQELVEEAIAY
 GRKLGGSQEDQIKNAIDKLFVLFGAEILKKIPGRVSTEVDARLSFDKDAMVÄRARLIELYKEAGI
 SKDRILIKLSSTWEGIQÄKELEEQHGIHCNMTLLFSFAQAVACAEAGVTLISPFGVGRILDWHVAN
 TDKKSYEPLEDPGVKSVTKIYNYKKFSYKTIVMGASFRNTGEIKALÄGCDFLTISPKLLGELLQD
 NAKLVPVLSAKAAQASDLEKIHLDÉKSFRWLHNEDQMAVEKLSDGIRKFAADAVKLERMLTERMFN
 AÉNGK

>TCPG

QTDIEITREEDFTRILQMEEYIQOLCEDI IQLKPDVVITEKGISDLAQHylMIRANITAIRRVRKT
 DNNRRIARACGARIVSRPEBLREDDVGTGAÄLLEIKKIDHEYFTFITDCKDPKACTILLRGASKEIL
 SEVERNLDQAMQVCRNVLLDPOLVPGGÄSEMAVAHALTEKSKAMTGVQWPYRAVÄQALEVIPRT
 LIQNCASTIRLLTSIRAKHTÖENCETWGVNGETGTLVDMKEI.GIWEPLAVKLQTYKTAVETÄVLL
 LRIDDIVSÄHKKKGDDQSROGGAPDÄGQE

>VIM

SPQRSSRAPTTÄTHRALVRLFSGSQSAPPSSPRPSPPSAAMSTRSVSSSSYRRMFGGPGTÄSRPS
 SSRSYVTTSTRYSLGSALRPSTSRSLYASSPGGVYATRSÄVRLRSSVPGVRLQDSVDFSLADA
 INTEFKNTRTNEKVELQELNDRFÄNYIDKVRFLÉQÖNKILLAELEÖLKQÖGKSRLGDLYEEEMREL
 RRQVDQLTNDKARVEVERDNLAEDIMRLREKLQEMLOREEEAENTLOSFRQDVDNAÅSLARLÄDLERK
 VÄSLQEEIAFLKKLHEEEIQELQAOQJOEÖHVQIDVDVSKPDLTAALRDVRQOYESVAÄKNLQHAE
 WYKSKFADLSEAAANRNNDALRQAKQESTEYRRQVQSLTCEVDALKGTNESLERQMREMEENFAVEÄ
 ANYQDTIGRLQDEIÖNMKEEMARHLREYQDLLNVKMA LDIEIATYRKILLEGEESRISLPLPNFSSL
 NLRETNLDLSPILVDTHSKRTLLIKTVETRDGQVNETSQHDDLE

>VIMC

QEEMLOREEEAENTLOSFRQDVNAÅSLARLÄDLERKVESLQEEIAFLKKLHEEEIQELQAOQJOEÖHVQ
 IDVDVSKPDLTAALRDVRQOYESVAÄKNLQHAEEWYKSKFADLSEAAANRNNDALRQAKQESTEYRR
 QVQSLTCEVDALKGTNESLERQMREMEENFAVEÄANYQDTIGRLQDEIÖNMKEEMARHLREYQDLL
 NVKMA LDIEIATYRKILLEGEESRISLPLPNFSSLNLRETNLDLSPILVDTHSKRTLLIKTVETRDGQ
 VINETSQHDDLE

Figure 6 (continued)

>ZHX1

EQTIINDLTDFGSFVKEENAEQAESTEVSSSGISISKTPIMKMMKNKVENKRIAVHHNSVEDVPEEK
ENEIKPDREEIVENPSS9SASESNTSTSIVNRIHPSTASTVVTTPAAVLPGLAQVITAVSAQQNSNLIP
PKVLIPVNSIPTYNAALDNNPLLNTYNKFPYPTMSEITVLSAQAKYTEEQIKIKIWFSAQRLKHGV
WTBEEVEEARRKQFNGTVHTVPQTITVIPHTISTGSNGLPSILQTCQIVGQPGVLTVQAGTNTLP
VTAPIALTVAGVPSONNLOKSOVPAOPTAETKPATAAVPTSQSVKHEITALVNPDSEFGIRAKKTKE
QIAELKVSYLNQFPHDSEIIRLMKITGLTKGEIKKWFSDTRYNQRNSKSNOCLHLNNNDSTTIII
DSSDETTEPTVGTAPQPKQSWNPFDFTPQKFKEKTAEQLRVLQASFLNSSVLTDDEELNRLRAQTK
LTREIDAWFTEKKKSALKEEKMEIDESNAGSSKEEAGETSPADESGAPKGSGSTGKICKKTPEQI
HMLKSAFVRTQWPSPEEYDKLAKESGLARTDIVSWFGDTRYAWKNGNLKWYYYYQSANSSSMNGLS
SLRKGRGRPKGRGRPRGRPRGSKRINNWDRGPSLIKFKTGTAILKDYYLKHKFLNEQDILDELV
NKSHMGYEQVREWFAERQRSELGIELFEENEEDEVIDDQEEDEEETDDSDTWEPPRHVKRKLSK
SDD

>ZNF33B

CYECGKTFCLKSDLTIHQRTHTGEKPFACPECGKFFSHKSTLSQHYRTHTGEKPYECHECGKIFYN
KSYLTKHNRHTGEKPYECNECGKTFQKSQQLTQHQRIHIGEKPYECNECGKAFCHKSALIVHQRT
HTQEKPYKCNECGK8FCVK9GLILHERKHTGEKPYECNECGKSFSHKSSLTVHYRAHTGEKSCQCN
ECGKIFYRKSDLAKHQRSHTGEKPYECNTCRKTFSQKSNLIVHQRTIGEKPYEC

Figure 6 (continued)

>ALEX2

GGCGAATCAGTAGTTGGGGCTGCAATGGCTTCTGCAATAGCACCACCTCCGGGTGACAGAGGCC
 CTTGGGGCTGCAAGCCCCCTGCAATGGCAGGGCTCCAAAGTGGCAGAAGCTCCCAGAGAGAAGCG
 GAGACTTCCAGGGCAGCGGTGCTCCTGGGACAGTGGTGCCTACCGAAGCGGCAGCACCACTGAG
 GTGACCGAGGGTCTGGGTAGCAGCACCTACCAAGGTAGCTGAAGCTCCGGGTGGCATCGCCT
 ACCGAGGCAGCTGAGGCTCCTGTGCCCAGCAACGCCTACTGGGGCTGAGCACCTACTGGGGCTGCA
 GAGCTCCTGGAACCTCTGGTCTCCCTAGAACAGCGGTGGTCTGGAACATCAGCTGCCAAGAAA
 GCAACCCCTGGGCTCACACTGGGCTATAACCGAAAGCCACATCAGGAGCTGGAGCGGTACCCAAA
 GGTGGAGGCAGGGTGAACCAAGGTCCCGGAATGGGGCAAGGGCAAGGGAAAGAAAAGCAAAAGTT
 GAAGTAGACGAACCTGGGATGGGCTTCCGTCTGGAGATGGGGCTGCAGCAGCTGCTGCAGCCTCT
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 AACAAATGCCAATTATTCAATGCAATCAAGAGACAAATCCGAAATTGGGAGGCCCTCCAATTATTGCA
 AACATGATCAACAAAATGATCCACACATTAAGGAAAAGCCTTAATGGCCATGAATAACCTGAGT
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 GACTACCAACACCTGCTTGTCAATTCCATTGCAAACCTTTCCGTTGCTATCTCAGGGAGGTGGA
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 CTTCTCAGTACCCAAAGTGCAGCATCTTAGTTCCCTCTATAATTCTACGTGGAATCAGAAATC
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 AGAGAATTCAATAAAGGTTCCCTTTTACTTATGCACATCTGGAGTGTGTTAAGAAAATT
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>APP1

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 ACCCCGAGGCCACAGACGGTGTGGATAATTACTTTGGCATGCCTGGGAAATCAGTGAGCACGAG
 GGGTTCCCTGAGGGCCAAGATGGACCTGGAGGAGCGTAGGATGCGCCAGATTATGAGGTGATGCGT
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 CACTTCCAGTCCATTCTGCAAGACTCTGGAGGAGCAGGTGTCTGGTGAAGCGACAGCGCCTGGTGGAA
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 GCAGCCCTGCAGGCAGATCCGCTCAGGGAGCGTGTCTGGCCCTGCGCGCTACCTGCGT
 GCGGAGCAGAAGGAACAGAGGCACACGCTGCCACTACCAGCATGTGGCCCGTGGATCCCGAG
 AAGGCACAGCAGATGCGCTTCAAGGTGCAACCCACCTCAAGTGTATTGAGGAGAGGGTGAATCAG
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 CTCCACTCTGAACACCTGGGTCCAGTGAATTGGAAGGCCCTGCCCTGGGGCAGCAGCGAGGAC
 AAGGGTGGGCTGCAGCCTCCAGATTCCAAGGTGACACCCCCATGACCCCTCCAAAAGGGTCCACA
 GAACAAGATGCTGCATCCCCTGAGAAAGAGAAGATGAACCCGCTGGAACAGTATGAGCGAAAGGTG
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 CTGGGACAGGGGTGCTCCGTGAGGCTGTGTGGGTCTGC

Figure 6 (continued)

>BAI P1

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 GTGGAGCGCTGAGAAGATCCAGAACGCTACAGCAAGGAATACAGTGACGACAAAGTG
 CAGCTGGCCATGAGACCTACGAGATCGGGATAAACACATCGAAGGCTTGATGCGACACCTGGCG
 CGCTTGAAGCAGATCTGAAGGACAAGATGGAGGGCAGCGATTGAAAGCTCCGGAGGGCGAGGG
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 GAAGACACACCAAGAAAAAGAACAAAGGAGGGTCTGAGTTCACTGACACCACTCTGCTCCGTG
 CACCCCTCTGATGTGCTGGACATGCCCGTGGACCCAAACGAACCCACGTACTGCCTGTGCCACCAG
 GTCTCCTATGGGGAGATGATTGGCTGTGACAATCCAGACTGTCCAATTGAGTGGTTCACTTGCC
 TGCGTGGACCTTACACGAAACCAAAGGAAAATGG

>BAI P2

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 TGCAACGCCATCCTCAAGTTGAGACGCCCTGACCATACAAGCTCGATCTCAGGCCAGTCC
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 GACCTGTTGACAAGTCTGGTGCAGTGCCAAACAGCAGCAGCAGCAGTAGCAGCAGCAACTCT
 CTTGTATCTGCAAGAAAATCCACCCAGAGACTGGGTATGTGTCGCAAGGAGATGGTATCTTC
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 GATGCCACGGAGTGAGTCTAGTACTGAATGGACTTAGATGGATTCACTGAGCTGGACTCTGAGTC
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 GATCAGCAGGGTTCTTG

Figure 6 (continued)

>BAIP3

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 ACCGGTTCCCAACTCTAAGCAGTATTTCACCAACTCAGATGTGTCACAACATAACATTCTCACG
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>BARD1

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 ACTTTAGCTGAAATCAACAAAATGAAATTAGAGGCAGAAAAAGAAGATGGTAATTGACTCC
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 GGAAAACGTGCCATCACAATAGACTTCCAGTCCCATTCTAAGAGATGTAGAACCCAGCATTCTG
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 TCACCACCTTCATGCAAACGTAAGTTGGTGGTACATCAGGGAGCAAACAGTAACATGTCGATG
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>CA150

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 GCAGTTCTGAATGGACTGAATATAAAACAGCAGATGGAAAGACATATTATAATAATAGAACA
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 AAG

Figure 6 (continued)

>CGI-125

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CCAGAATATGCCAAGTATCTAAAGTAGGCTCAGTGTGTTACGACGCTTAGAGGTGCTGAAATATGAA
 CACTTCCGAAGGAGCTGGTGAATGCTCAGTGTGCGAAATTATTGATGAAACAGCAGATTCTACAT
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>CGI-74

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 GACAGAAGCACTGGCTGATCATTGGGGTAAACTGCACCTGGATTATTGAAATAAGAGAGAAAG
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 AGAGAAG
 AAAAGG

>CLH-17

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 CTTGAGACT

>CLK1

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 GAAGCCTTAAAGCATCCTTCTTGACCTCTGAAGAAAAGTATA

Figure 6 (continued)

>DRP-1
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GAAGACGGAAACATCAACGTCATCAGGCCATGCCGCTTCATTCCGCGGAAGGCAGTCCCGGAG
CACCTGTACCAAGCGCGTCAAAATCAGGAATAAGGTTTGAGTCAAGGGTTCCAGGGCATG
TATGACGGTCTGTGTACGAGGTACCCAGCTACACCCAAATATGCAACTCCGCTCCTCAGCCAA
TCTTCGCCCTCTAAACACCAGCCCCCACCACATCAGAAACCTCCACCAGTCCAACCTCAGCTTATCA
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CGCTCCAACATCACCAAGCCTCGGT
>EF1A
ATGCACCATGAAGCTTGAGTGAAGCTCTCCTGGGACAATGTGGCTCAATGTCAAGAATGTG
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GCTGCTTCAGTGCCTCAGGTGATTATCCTGAACCATCCAGGCCAAATAAGGCCGGCTATGCCCT
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CGTTCTGGTAAAGCTGGAAGATGGCCCTAAATTCTTGAAGTCTGGTGAATGCTGCCATTGTTGAT
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GTTCTGTATGAGACAGACAGTTGCGTGGGTGTCATCAAAGCAGTGGACAAGAAGGCTGCTGGA
GCTGGCAAGGTACCAAGTCTGCCAGAAAGCTCAGAAGGCTAA
>EF1G(bait)
GCGGCTGGGACCCCTGTACACGTATCCTGAAAACGGGCTTCAGGCTCTCATCGCTGCTCAG
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ACCCCTGAATTCTCCGCAAATTCTCTGCCGGCAAGGTCCCAGCATTGAGGGTGTGATGGATT
TGTGTGTTGAGAGCAACGCCATGCCTACTATGTGAGCAATGAGGAGCTGCCGGAAAGTACTCCA
GAGGCAAGCAGCCAGGTGGTGCAGTGGTGAGCTTGCTGATTCCGATATAGTGCCAGGAG
ACCTGGGTGTTCCCCACCTTGGGCATCATGCACCACAACAAACAGGCCACTGAGAAATGCAAAGGAG
GAAGTGAGGCCAATTCTGGGCTGCTGGATGCTTACTTGAAGACGAGGACTTTCTGGTGGCGAA
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Figure 6 (continued)

>EF1G (prey)

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 GCAGAGACCCAACCTAAAAAGGACACACCACGGAAAGAGAAGGGTTCACCGGAAGAGAAGCAGAAG
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 TGTGAGCAGGCCTGGCTGCTGAGGCCAAGGCCAAGGACCCCTCGCTCACCTGCCAAGAGTACC
 TTTGTGTTGGATGAATTAAAGCGCAAGTACTCCAATGAGGACACACTCTGTGGCACTGCCATAT
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 AAGAATGCCTTCGCCAGTGTCACTCTTTGGAACCAACAATAGCAGCTCCATTCTGGAGTCTGG
 GTCTCCGAGGCCAGGAGCTGCTTCCGCTGAGTCCAGATTGGCAGGTGGACTACGAGTCATAC
 ACATGGCGGAAACTGGATCCTGGCAGCGAGGAGACCCAGACGCTGGTTCAGAGTACTTTCTGG
 GAGGGGGCCTTCAGCATGTGGCAAAAGCCTCAATCAGGGCAAGATCTCAAG

>FEZ1

GGCAACTGCTCTGACACTGAGATCCATGAGAAAGAAGAGGAAAGAGTCAATGAGAAGAGTAAAAT
 GATTCCGGTATCAACGAGGAGCCTCTGCTCACAGCAGATCAGGTAAATTGAGGAGATTGAGGAAATG
 ATGCAGAACTCCCCAGACCCCTGAGGAAGAAGAGGAGGTTCTGGAAGAAAGAGGATGGAGGAGAAA
 ACTTCCTCCAGGCAGACTCGGTCTCTGCAGGAGATGCAGGCATTGACACAGACCTCAACAAAC
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 GGTGCCATCCGTGACTCTCGGAGGAGCTGGTGCAGCAGCTGGCCCGCCGGACGAGCTGGAGTT
 GAGAAGGAAGTGAAGAAACTCCTTATCACGGTCTTATTGAGGTTCAAGAACAGCAGAAGGAGCAG
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>G45IP1

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Figure 6 (continued)

>G45IP2

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 GCGGAGGAAGCCGCCGTGGAGGGATCTGGTCCGCAAAGTCTGGCATCCTACTGGAGACAGCC
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 GGCGCCCTGAAGGAGCTCAGCAAGAGGCTCAACCACAGGAATTATCTCTTGGAAATCTCCGCATAGG
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 GAATTTCGCCTCCAGCATGTCCTACCACTGCGACCTGTGCACCCAGCGCGGCTCATCTGCAGATC
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>G45IP3

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 AATCCTATTATTACCTCAGAAGTTTTCTCGCAGGATTTCGACGCTTACCACTCCAG
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 AGAAGTCCCACCTCTAAACACATCCGTATTACTCGCATCAGGAGTATCAATCACCTGAGCTCACCA

>GADD4.5G

GGTGCAGGGCTGAGCCGGGATTGGAGTGTGGTGGAGTTGGGGAGCCAAGGGTGTGCGCGGTGG
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 ATGCAGGGTGCCGGAAAGCGCTCATGAGTTGCTGTCGGCGAGCGTCAGGGCTGCCTCACT
 GCCGGCGTCTACGAGTCAGCAAAGTCTTGAACGTTGACCCCGACAATGTGACCTTCTGTGTGCTG
 GCTGCGGGTGAGGAGGACGAGGGGAGACATCGCGCTGCAGATCCATTACGCTGATCCAGGCCTTC
 TGCTGCCAGAACGACATCGACATAGTGCCTGGCGATGTGCAGCGGCTGGCGGCTATCGTGGGC
 GCCGGCGAGGAGGAGGCGGGTGCCTGGGGCACTGCACTCATCTCATTGAAACCCAACGAGGAC
 GCCTGGAAGGATCCCCCTTGGAGAAGCTCAGCCTGTTGCGAGGAGAGCCGCAGCGTTAACGAC
 TGGGTGCCAGCATCACCCCTCCCCGAG

Figure 6 (continued)

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>GIT1
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TATGACGAGGTGGATCGAAGAGAAAATGATGCAGTGTGGCTGGCTACCCAAAACCACAGCACTCTG
GTGACAGAGCCAGTGCCTGCCTGTTAACCCGGAATACTCAGCCACGCCAAATCAG
GGCCGACAAAAGCTGGCCCGCTTTAATGCCCGAGAGTTGCCACCTTGATCATGACATTCTGAGT
GAGGCCAAGCCGAGACAGCAGGCCAAGAGCCTGAGCAGCCCCACAGACAACCTGAGCTGTCTCTG
CGGAGCCAGAGTGCACCTCGACGACCAACACGACTACGACAGCGTGGCTCTGACGAGGACACAGAC
CAGGAGCCCCCTCGCAGCACCGGCCACTCGGAGCAACCGGGCCCGAGCATGGACTCCTCGGAC
TTGCTGACGGGGCTGTGACGCTGCAGGAGTACCTGGAGCTGAAGAAGGCCCTGGCTACATCGGAG
GCAAAGGTGCAGCAGCTCATGAAGGTCAACAGTAGCCTGAGCGACGAGCTCCGGAGGCTGAGCGA
GAGATCCACAAGCTGCAGGCCAGAACACACACACCCATGGCCAGGGGGAGCACACACCGCAGGGAT
CCACTCCCCAGTGAACCGGCCAGAACACACACCCATGGCCAGGGGGAGCACACACCGCAGGGAT
CGCCAGGCCCTTTCCATGTATGAACCTGGCTCTGCCCTGAAGGCCCTTGGGGGCCCTGGGGAC
GAGCTCACTACGCCGCTGCAGCCTTCCACAGCACTGAGCTAGAGGACGACGCCATCTATTCACTG
CACGTCCTGCTGGCCTTACCGGATCCGGAAAGGGGTGTCGCTCAGCTGTGCCCTTCACTCCC
TCCTCCCCGGCTGCTGTCCTGCTCCAGGAGGAAGCCCAACAGAGCAAGCTTCCGCCACGGC
AGTGGAGCCGACAGTGAATGAGAACACGCCAAAGTGGGACCCACTGCTGGGCTGGAAGGGAAAG
AGGTTCTAGAGCTGGCAAAAGAGGAAGACTTCAACCCAGAGCTGGAAAGCCTGGATGGAGACCTA
GATCCTGGGCTTCCCAGCACAGAGGATGTCATCTGAAGACAGAGCAGGTACCAAGAACATTCA
GAACGTGCGGGCAGGCCAGGGAGTTCAAGCATGACAGCTCGTGCCTGCTCAGAGAACATCCAT
TTGGCTGTGACCGAGATGGCCTCCCTTCCCAAAGAGGCCAGCCCTGGAGGCCAGTGCAGGAGCTCA
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CCCAGGCCCTGGACTTCCAGCTGACTCAGCAGGTGATCCAGTGCCTATGACATGCC
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>hADA3
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GAGCTCGCAAACGGCAGGCTGAGCTGAAGGCACCTAGTGCCTACAAACCGCACCAAGAACGAC
CTGCTGAGGCTGGCAAAGGAGGAGGTGAGCCGGCAGGAGCTGAGGAGCCGGTGCATGGCTGAC
AACGAGGTGATGGACGCCCTTCGCAAGATCATGGCTGCCCGCAGAAGAAGCGGACTCCCACCAAG
AAAGAAAAGGACCAAGGCCCTGGAAGACTCTGAAGGAGCGTGAGAGCATCCTGAAGCTGCTGGATGGG

```

Figure 6 (continued)

>HBO1

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 CGCCGGCAATGCCGCGAAGGAAGAGGAATGCAGGCAGTAGTTAGATGGAACCGAAGATCCGAT
 TTTCTACAGATCTCGAGCACACAGACAGTTAGAAAGTGAAGGCACATCCGACGATCTGCTCGA
 GTCACCCGCTCTCAGCCAGGCTAAGCCAGAGTTCAAGATTCCAGTCTGTGCAAGAATGCTCGA
 TCTTTGGCAGTGAGGAGCTGGTTACCTACCAAGAGTGACCCGTAGTCAGCAGCAGCCTACC
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 AGCATTGCCAAGGACATGTCCTGAAGGACTCAGGCAGTGATCTCTCATCGCCCCAAGGCCGT
 CGCTTCCATGAAAGCTACAACCTCAATATGAAAGTGTCTACACCAGGCTGTAACCTCTAGGACAC
 CTTACAGGAAAACATGAGAGACATTCTCATCTCAGGATGCCCACTGTATCATAACCTCTCAGCT
 GACGAATGCAAGGTGAGAGCACAGAGCCGGATAAGCAGATAGAAGAAAGGATGCTGTCTCACAGG
 CAAGATGACAACAACAGGCATGCAACCAGGACCAGGACCAACGGAGAGGCAGCTCGATAAAG
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 GGCAAATCACAGAGGGAAAGCAACATGATTAACAAATTGCTTTGGCGCTATGAGCTTGATACC
 TGGTATCATTCTCCATATCCTGAAGAATATGCACGGCTGGGACGTCTCTATATGTGTGAATTCTGT
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 GTGGAGCCCTCCTGTTCTATGTATGACAGAGGCGGACAACACTGGCTGTCACCTGATTGGATAT
 TTTCTAAGGAAAAGAAATTCACTCCCTCAACTACAAACGTCTCTGTATCTTACTATGCCTCAGTAC
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 GTTGGCTCCCCAGAACGTCCACTCTCAGATCTGGGCTTATAAGCTATCGCAGTTACTGGAAAGAA
 GTACTTCTCCGCTACCTGCATAATTTCAGGCAAAGAGATTCTATCAAAGAAATCAGTCAGGAG
 ACGGCTGTGAATCCTGTGGACATTGTCAGCACTCTGCAAGCCCTCAGATGCTCAAATACTGGAG
 GGAAAACACCTAGTTAAAGAGACAGGACCTGATTGATGAGTGGATAGCCAAGAGGCCAAAGGGCAAAAGG
 TCCAACCTCAATAAACCATGGATCCCCAGCTGCTTAAATGGACCCCTCCCAAGGGCACT

Figure 6 (continued)

>HD1.7

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 CCGCCGCCGCCGCCCTCCTCAGCTTCCTCAGCCGCCGCCAGGCACAGCCCTGCTGCCCTCAG
 CGCAGCCGCCGCCGCCGCCAGCCACCCGGCCGGCTGAGGAGCCCTGAC
 CGACCAAAGAAAGAACTTCAGCTACCAAGAAAGACCGTGTGAATCATTGCTGACAATATGTGAA
 AACATAGTGGCACAGTGTGAGCAGGAAATTCTCCAGAATTCTAGAAACTCTGGGCATCGCTATGGAA
 CTTTTCTGCTGTGCAGTGATGACGCAGAGTCAGATGTCAGGATGGTGGCTGACGAATGCTCAAC
 AAAGTTATCAAAGCTTGTGATGGATTCTAATCTTCCAAGGTTACAGCTCAGGCTTATAAGGAAATT
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 GTGACCGGAGGCCCTGGAGCTGTTGCAAGCAGCTCTCAGAACGCCCTCACCCGAGCTCTGCAAACC
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 GTCAGCAGCTGCTCTAACAGCCTCAGTGAAGGATGAGATCAGTGGAGAGCTGGCTGCTCTTCA
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>HDD1.0

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 CGCAGCCGCCGCCGCCGCCAGCCACCCGGCCGGCTGTGGCTGAGGAGCCGCTGAC
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 GTTGGCCCTCAGAAATGCAAGGCTTACCTGGCTGAGCTGTTCCAAAATTATGGCTTCTTGGC
 AGACCCGAAGAATCAGTCCAGGAGACCTTGTGCTGAGCTGTTACAGAACAAAGCAAG
 AATTGGCAAATGACAATGAAATTAAAGGTTTGTAAAGGCCCTCATAGCGAACCTGAAGTCAAGC
 TCCCCCACCATTGGCGGACAGCGGCTGGATCAGCAGTGAGCATCTGCCAGCAGCAAGAAGGACA
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Figure 6 (continued)

>HDd1.3

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 AACCTTCTGCCGTGCTGACTCGAACAGCAAGAGAGACCCGAAGAATCAGTCCAGGAGACCTGGCT
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TTAAGGCTTCATAGGAAACCTGAAGTCAGGCTGGGACAGGGCTGATCA
 GCAGTGAGCATCTGCCAGCACTCAAGAAGGACACAATTATTCATAGTGGCTACTAAATGTGCTC
 TTAGGCTTACTCGTTCTGAGGATGAACACTCCACTCTGCTGATTCTGGCGTGCTGCTCACC
 CTGAGGTATTGGTGCCCTGCTGAGCAGCAGGTCAAGGACACAAGCCTGAAAGGCAGCTCGGA
 GTGACAAGGAAAGAAATGGAAGTCTCTCCTCTGAGAGCAGCTTGTCCAGGTTATGAACGTGAGC
 TTACATCATACACAGCACCAAGACCACAATGTTGTGACCGGAGCCCTGGAGCTTGCAGCAGCTC
 TTCAGAACGCCCTCACCCGAGCTCTGCAAACCCCTGACCGCAGTCGGGGCATTGGGAGCCTCACC
 GCTGCTAAGGAGGAGCTGGTGGCGAAGCCGTAGTGGAGTATTGTGGAACTTATAGCTGGAGGG
 GGTTCCCTCATGAGCCCTGTCCTTCAAGAAAACAAAAGGCAAAGTCTCTAGGAGAAGAAGAA
 GCCTTGGAGGATGACTCTGAATCGAGATCGGATGTCAGCAGCTCTGCTTAACAGCCTCAGTGAAG
 GATGAGATCAGTGGAGAGCTGGCTGCTTCAAGGGTTTCACTCCAGGGTCAAGCAGGTCAATGAC
 ATCATCACAGAACAGCCACGGTCACAGCACACTGCAGGGACTCACTGGATCTGGCAGCTG

>HDexQ20

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 CCG

>HDexQ51

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 CAGCCGCTGCTGCTCAGCCGAGCCGCCGCCGCCGCCACCCGGCCGGCTGTGT
 CTGAGGAGCCGCTGACCCGACCGTGAAGTCGAC

>HIP1

GCTGACACCCCTGCAAGGCCACGGGACCGCTTATGGAGCAGTTACAAAGTTGAAAGATCTGTT
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 CCCAACCTCCCTGCGAGCCTCAGCCCTGTCAGAACATATCAGCCCTGTTGATCCCTGAGAG
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 TTGAAGCAGGAACCTGGCACAAGCCAACGGGAGCTCAGGTTCTGCAAGGCAGCCTGGAAACTTCT
 GCCCAGTCAGAACAGCTGGCAGCCGAGTTGCGCAGCTAGAGAAGGAGCAGGGACAGCCTGGTG
 AGTGGCGAGCTCATAGGGAGGAGGAATTATCTGCTCTCGGAAAGAACTGCAGGACACTCAGCTC
 AAACAGGCCAGCACAGAGGAATCTATGTGCCAGCTGCCAAAGACCAACGAAAATGCTCTGGTG
 GGGTCAGGAAGGCTGCCAGGTGATACAAGACGCCGTCAGCGGCCG

Figure 6 (continued)

>HIP11

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 GTGGACGTGGTTGGCTGCCGATGTAGAACACTGCAGCGCCTGCCAAGGTATCGGGAAACCAG
 AGCCTGGTCAACGAGCTGGCCTCACCGCCCGAAGATGATGGCTGACGAGGCCCTGGCAGTGGG
 CTGGTCAAGCCGGTGTCCAGACAAAGAGGTATGCTGGATGCTGCCCTAGCGCTGGGGCCGAG
 ATTCCAGCAAGAGCCCCGTGGCGGTGAGAGCACCAGGTCAACCTGGTATTCGGGACCAT
 TCGGTGGCCAGAGGCCCTCAACTACGTGGCTCTGGAACATGAGCATGCTGAGACCCAAGACCTC
 GTGAAGTCGGTCCAGGCCACGACTGAGAACAGGAACGTAAAACGTCACCTCTCCAAGCTC

>HIP13

CCCTGCTGCTCTGAGGACACCATCCCTCCAAGTTTCAAGATTATGATTATTCCTGTAAAGTGGT
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 CAGTCCTACCGACGGATGTTCCAAGGCCAAGCGTCCAGCCTCAACTGCTGGCTCCCCACCAACCCCTG
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 ACCGTCCCAGACCTCCAGGGGTGTTGCAGCCCTCCAGATGGGCCAGAAGAGCGGGGGAGCAC
 AGCCCTGAGTGGCATCTGTTGAGGGCCCCAAGGTGTCACCAGCATGCCCTCCTCAATGTGG
 AGCGGCCAAGCTTCCGTTAACCCCTCCACTTCCAGGCCGAAGCCCAGTATCCGTAGGGAGCACAGA
 CAGGCAATTCCAGAAAGTGAAGCTGAAGACCAGGAACGGGAAACCCCCAAGTGCACACTGTCTCCCCA
 GGCAGATTCCAGAGAGTGAACCTGAGACCTGAGGCCAAGGGATACTCCACAAGGAGAACATG
 CTGAACGCCATCCGAAGGGCGTGAAACTGAAGAACGACAAACGATCGCTCAGCCCCCTCGC
 TTTCT

>HIP15

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 ACAGCCAATGCGAGAAGCAAGTTCACGTTCTGAAAATGCTATTGAATTGTCTGAAAATCCTGCT
 GTGGCAAAAAACTATTCACTGGCAAAGCTCTTCAATATTGTGGGCTCTTAAACATAGAAGAG
 ACAAAATGATAATTCAAATTGTTATTAAAATGTTCAGAATATCAGTAACATTATAAAAGTGGG
 AAGATGTCCTTAATTGATGATGATTTCAGTCTTGAGCCGCTTATTCTGCATTGTAATTGAG
 GAGTTAGCTAAGCAACTACAAGCCAAATAGACACCAAAATGATCCTGAGGTGGACAACAAAGT

>HIP16

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 GATTCTTGAAAGAGAAGAGGGAAAGCTGTGGAGGGAGTAAGCCAAAGGACGTGGACCTGACACTA
 CCTGGCTGGGGCAGTGGGTGGCTCAAAGCCAGTGCACAGGAAAGACGCCGTTCTC
 ATTAAGCCCTGAGGGTCTCCAAGAAAAGATAAGAATTGCAAATGTGATTATCAATGAGAAG
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 TTTGAAAGGACCATCCAGACCCCCATAGGATCCACATGGAACACCCAGAGGGCTTCCAAAAGCTG
 ACTACTCCCAAGGTGTCACCAAGCCAGGCCATATCATTACCCATAAAAGCAGAACGACGTGGG
 TACCGGCTTCTCTCAAGGTGCGACCTGTCATACAGAGGAATCCAAAACGAATCACCACACGT
 CACAAAAACAGCTGAAGAAATGCTCTGTAGAT

>HIP2

ATGCCAACATCGCGGTGAGCGAATCAAGCGGAGTTCAAGGAGGTGCTGAAGAGCGAGGAGACG
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 GGACCTCCAGACACACCATATGAAGGAGGAAGATACCAACTAGAGATAAAAATACCGAACACATAC
 CCATTAACTCCCCCTAACGGTCCGGTTATCACTAAAATATGGCATCTAAATTAGTTCGGTCACA
 GGGCTATTGTTGGATATCCTGAAAGATCAATTGGCAGCTGCAATGACTCTCCGACCGTATT
 TTGTCATTGCAAGCACTATTGGCAGCTGCAAGCAGATGATCCACAGGATGCTGTAGTAGCAAAT
 CAGTACAAACAAAATCCGAAATGTTCAACAGACAGCTGACTTTGGCACATGTGTATGCTGGA
 GCACCAAGTTCTAGTCCAGAAATACACCAAAATAGAAAACCTATGTGCTATGGGCTTGTAGAGG
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 AGTAACGT

Figure 6 (continued)

>HIP5 (bait)

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 GAAAAGGTGCAGAAATTCAAAGACTATTAAAAACTGAGGTGGTTGATGAAACTAGCAATATA
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 GCCTCAAAAAAGAAGAAAGTAAAATCCCTGTACATGATGATTCTAAACTAAGCAAGGTAAAGCCA
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 ATACAAGTGTCTCAGTGTCAAGGAGTAACCTCTGAAATCCTCAAACATTACACATAACTCT
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 GAGTGCCTAAACTTGCCTAAATTAAATCATTCAAATGGCACTCAAGCAGTTGCCGGCAAGATGCC
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 GATAGTACTTCTGAGTTTTGATGGCTGAAAATTAGTGAAGCATTAGTGCCTGATCAAATAAGAGGCT
 CTGACTGTCTGAAATACCAAACAGATAAGAAATCAAATCTACCTTAAATAAAACTCAACAAATT
 AACATCTGCACACTGTGTCAGCTGAAAGAACAGAAGATCCTAGAGTCCCTTAATGATCTCAATGAAAGA
 CTACATTATATAAGAATCCATTGCAAAACCCATCCATCAAATAACTTTACAAATAATACCA
 CTTCTGGAGAAGAGAGAAGATAGAACCGAGCAGCTGAGAGACAAGAGA

>HIP5 (prey)

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 CTTCTGGAGAAGAGAGAAGATAGAACCGAGCAGCTGAGAGACAAGAGA

Figure 6 (continued)

>HMP

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 GAGGGTGCATTGAAGGAACGCAGAAAGGCAGTAGATGAAGCTGCCATGCCCTCTCAAAGCCAAA
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CCTCATATAACTGCTGCAGAGGGTAAACCTCACACATGATAGTTGATCTGGATAATGTGGTCAAA
AAGGTCCAAGCAGCTCAGTCTGAGGCTAAGGTTGATCTCAGTATCATGAGCTGGTGGTCCAAGCT
CGGGATGACTTTAACGAGAGCTGGACAGTATTACTCCAGAACATGCTCTCTGCTGGTGGAAAGGAATG
AGTGTTCAGACTTAGCTGACAAGCTCTACTGATGATCTGAACTCCCTCATGCTCATGCACAT
CGTCGTATTGATCAGCTAACAGAGAGCTGGCAGAACAGAACAGGACACCGAAAAGCAGCACATCACG
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CTTAGGGTACAAGAACAGGAATTGAAAGTCTGAATTGAGCAGAACCTGCTGAGAAACTCTCTGAA
CAAGAATTACAATTTCGTCGTCTCAGTCAGAACAGAACAGTTGACAACACTTACTCTGGATATAAAACT
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CTGAAGCCGCCAGAGCTCTGCCCTGAGGATATAAACACATTAAATTACTGTCATATGCTTCC
TATTGCAATTGAGCATGGTGTACCTGGAGCTAGCAGCAAAGTTGTCATGCAAGCTGAAGGGGGAAATCC
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>HP2 8

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 TTGATCCGGGAGGTCAACATCAACTGTGCGGAGAGGGGCTGCTGCTGCTGCCAGTCCGGGACGAG
 ATCCGCATGACCATCGCTGCCCTACCAAGACCCCTGTACAGAGAGCAGCGTGGCGTTGGCATGAGGAAG
 GCACTGCAGGCTGAGCAGGGAAAGTCAGACATGGAGAGGAAAATCGCAGAACATTGGAGACGGAAAAG
 AGAGACCTGGAGAGGCAAGTGAACGAGCAGAACAGGAAAATGTGAAGGCCACTGAGAACGGGGAGAGC
 GAGAGGGGGCAGGTGGAGGAGAAGAACAAATGAGGAGATTCAAGTCCCTGAAGCGAACAAATCAG
 CAGCTGAAGGCCAACTGGAAGGCATTATTGCACCAAAGAAG

Figure 6 (continued)

>HSPC232

CGGCGGCGAGCGGACGGCTGCATTTACGGGGTCTCCGGAGGGCCAGAGTCGGCTTACAGAAGA
 GACGAAATGTGGTCTGAGGGACGATATGAATATGAAAGAATTCCGAGAGAACGAGCACCTCCTCGA
 AGTCATCCCAGTGTGAAATCTGGTTATAGATGGACAAGAGAGCGATCATTCTGCAAGCAGGAAACCT
 GAATACAGGGACATGAGAGATGGCTTAAAGAAAAAGTTCTACTCTTCCATTATGCGAGAGAG
CGGTCTCCTTATAAAAGGGACAATACCTTTTCAAGAGAATCACCTGTGGCCGAAAGGATTCTCCA
CAACAGAGATCTGGTCCAGTGTCAAGTAGCAGAAGCTACTCTCAGAAAGGAGAAATCATACTCT
TTCCATCAGTCTCAACATAGAAATAAAGAGAGGCCGTCCAGTCTTAAAACATCAAGAGAATACT
TCACCCCTCAAGTGGTCTAGCAGTTCTCATCAAAGGTGTTAGACAAACCCAGTAGGCTAACTGAA
AAGGAACCTGCTGAGGCTGCAAGCAAGTGGCTGCTGAAAAGCTAGAGAAATAGATGAAAGTAAC
TTGCTGAAATTCTGAGTATGAGGCGGGATCCACAGCACCATTGTTACTGACCAGGCCAGGAA
CCTGAGTCACACACATGGATAGAATTATTGAAAGATAGTCAGCTAACACTCGCTCTAAA
GCAATAGCATCAAAACCAAGAGATTGAAACAGGTTACCGACAAGACTGTGAAACTTCCGGATG
GTGGTGAAATGCTGATTGAAAAGATCCTCATAGAAAAGTCTATACAGTTGATTGAGGAG
AATTACATGAAATAGGTGAGCGGTGTTGAAAGAACTCAAGCATTGAGAGTATGATACT
TCCACTCAAGATTGGAGAGCCTTT

>HYPA

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 CAGTCTACCTGGGAGAAACCGAGATGATCTTAAACACCTGCTGAGCAACTCTTATCTAAATGCC
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 TGGGCCAAACCTAAAGAACTTGAGGATCTGAGGATACCAGAAATACCATTGTTGCTGAAAGTCTT
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 AAAAGAAAAAA

>HZFH

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 CGGGCCTACCCGCCGGTCCCTACGCTACACCTCCGGGGTACGGGGCGGCCCTCAGGCCAGGCC
 GTAGGGGCCCTGGCCGCCAGGCCAAATTACAGCCAGATGCTGCAAGGGTCTCATCACAGCC
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Figure 6 (continued)

>IKAP

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 ATTTGGACTCTTACTTACAGCAGAATTACAGCTACCCGGTCTAGGTCCCAATTCTACTGCAAAT
 AGTATCATGGCATCTTATCAGCAACAGAAGACTTCGGTTCCCTGTTCTGATGCTGAGCTTTTATA
 CCACCAAAGATCAACAGAAGAACCCAGTGGAGCTGAGCCTGCTAGAC

>IMPD2

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 ACCAAGAAAATCACTCTTAAGACCCCCACTGGTTCTCTCCATGGACACAGTCACAGAGGCTGGG
 ATGGCCATAGCAATGGCCTTACAGGCGTATTGGCTTCATCCACCACAAGTACACCTGAATT
 CAGGCCAATGAAGTTCGAAAGTGAAGAAATATGAACAGGGATTCAACAGAGACCCCTGGTCTC
 AGCCCCAAGGATCGGGTGGGGATGTTTGAGGCCAAGGCCCCGATGGTTCTGCGGTATCCCA
 ATCACAGACACAGGCCGGATGGGGAGGCCGTTGGTGGGCATCATCTCCTCCAGGGACATTGATT
 CTCAAAGAGGAGGAACATGACTGTTCTGGAAGAGATAATGACAAAGAGGAAAGACTTGGTGGT
 GCCCCTGCAGGCATCACACTGAAGGAGGCAAATGAAATTCTGCAGCGCAGCAAGAAGGAAAGT
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 GACTACCCACTAGCCTCCAAAGATGCCAAGAACAGCTGCTGTGGGGCAGGCATTGGCACTCAT
 GAGGATGACAAGTATAAGGCTGGACTTGCCTGCCAGGCTGGTGTGGATGTAGTGGTTTGACTCT
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Figure 6 (continued)

>KPNB1

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>KU70

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 TCCCTGTCGTGTACCCAGAGGAGTCGCTGGTATTGGAGCTCAACCTGTTAGTGCCTGCTC
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>LUC7B1

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 CAGGATCGCTTGAGGAGAGAGGAGAGGGAACGGGAGGGCTTGAGCAGGAGGTGGGATCA
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>MAGEH1

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Figure 6 (continued)

>MAP11c3

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 TTCGGCTTC

>mHAP1

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 CCCGGCGTGTCCGGCCTGAGCGTGCAGGCTTATTCGAGAGCTGCAGGAAGCGTTGTCTTAAT
 CCACCAACCCACGAAGAAGATCACCGAAGATGATGTCAAAGTGTATTTGCTGGAAGAGAAA
 GAACGGGACCTGAACACAGCCGCCGGATCGGCCAGTCCCTGGTAAACAGAACAGTGTCTTGATG
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 GACGAGGAAGACGAGGAAGAGGGCGAAGAGGAGAACAGAGAACAGAGGATCAAGACACAGCAG
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Figure 6 (continued)

>NAG4

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GCTGACTTGCAAGAAAATCGAAAGCAGAAAGATGGAACAGACACCTCACAGAGTGGGAGGACGG
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AAAGAAAATAAAAGAAAGACAAAGATATGCTGAAGATAAGTTAAAAGCAATAATTAGAGAGA
GAGCAGGAGGAGCTGACCGCATCGTGAAGGAATCTGGAGGAAAGCTGACCAAGGGCTTGTGAAC
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GATCCCATTGTAGGAGAGCCAGGCTACTGCCCTGTGAGACTGGGAATGACAACCTGGAAAGACTTCAG
TCTGGAGTGAATACTTGTGAGGGTTCAAAAGAGGATAAAAGGAACAAAGTCACTCCAGTGTATAT
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CATGAGTTTTGGCCACGTGCCAAGATTATCGTATGTCAAGGAGATAGTTACTGGATGTTTA
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CCCGTCATGGAAAACAACTTGTGGATTTGACAGAAGACACTGAAGAACCTAAAAAGACGGATGTT
GCTGAGTGTGGACCTGGTGGAAAGT

Figure 6 (continued)

>NEFL

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 CCAGAGGCTGCTCCCCCGTGGCCCTGCACCAAGCAGCTCCTACACCGGCCGGCCCTGCACCCAGCC
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 CTGGGCTTCTGCATTCTGGACAGCCAAGTCTGACTTCACGTACTCCCCCTGCCCTCAACAAG
 ATGTTTGCCAAGTGGCAAGACCTGCCCTGTGCAGCTGTGGGTTGATTCCACACCCCCGCCGGC
 ACCCGCGTCCCGGCCATGGCCATCTACAAGCAGTCACAGCACATGACGGAGGTGTGAGGCGCTGC
 CCCCCACCATGAGCGCTGCTCAGATAGCGATGGCTGGCCCTCTCAGCATCTATCCGAGTGGAA
 GGAAATTGCGTGTGGAGTATTGGATGACAGAACACTTTGACATAGTGTGGTGTGCCCCCTAT
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 CTGGGACGGAAACAGCTTGAGGTGCGTGGTGTGCCCTGGAGAGAACCGGCCACAGAGGAA
 GAGAACATCTCCGCAAGAACAGGGAGGCCTCACCAAGCAGCTGCCAGGGAGCACAAAGCAGACTG
 CCCAACAAACACCAGCTCCCTCTCCCCAGCCAAGAACAGAACACTGGATGGAGAACATTTCACCC
 CAGATCCGTGGCGTGAGCGCTCGAGATGTTCCGAGAGCTGAATGAGGCCCTGGAAACTCAAGGAT
 GCCCAGGCTGGGAAGGAGGCCAGGGGGAGCAGGGCTCACTCCAGCCACCTGAAGTCCAAGAACGG
 CAGTCTACCTCCCGCATAAAACTCATGTTCAAGACAGAACAGAACGGCCTGACTCAGAC

Figure 6 (continued)

>PFN2

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 TGGCAGCCACGGCAGGGGGCGTCTTCAGAGCATTACGCCAATAGAAATAGATATGATTGTAGGA
 AAAGACCGGGAAAGGTTCTTACCAACGGTTGACTCTGGCGCGAAGAAATGCTCAGTGTACAGA
GATAGTCTATACTCGATGCTACTGCCAAATGCCACATCGGGACAAAGAGTCAGGTGGGAGCCA
 ACATACAATGTGGCTGCGCAGAGCTGTTAGAGTCTTGGTCTTGTAATGGAAAAGAACGGGTC
 CATGGAGGCCGATTGAATAAGAAGGCATACTCAATGGCAAATACTTGAGAGACTCTGGGTTTC

>PIASy (bait)

CTGGTGGAGGCCAAAAACATGGTGTAGAGTTTCGAGTCTCCGACCTTCAGATGCTCTGGGTTTC
 GTGGGCCGGAGTAAGAGTGGACTGAAGCACGAGCTCGTACCCAGGGCCCTCCAGCTGGTGAGTT
 GACTGTAGCCTGAGCTGTTCAAGAAGATCAAGGAGCTGTACGAGACCCGCTACGCCAAGAAC
 TCGGAGCCTGCCCCACAGCCGACCGGGCCCTGGACCCCGTACCGTACCTACCCACCTAC
 GCCGGCGCTGTGCCAGGACTCCGCTGGCAGGCCCAATATTGACTACCCGTGCTACCGAAAG
 TACTTAAACGGACTGGGACGGTTGCCAGAACACCTCAAGCCAGAACGCTCCGCTGGTAAGCTG
 CCGTTCTTAAATATGCTGGATGAGCTGCTGAAGGCCACCGAATTAGTCCCACAGAACACGGAGAAG
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 GGCTACTACCCCTCCAATAAGCCGGGGTGGAGGCCAAGAGGCCGTGCCGCCCCATCAACCTCACT
 CACCTCATGTACCTGTCCTGCCACCAACCGCATCACTGTACCTGGGGAACTACGCCAAGAGC
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 AGCGAGATGCCACCAACGGGTGTGCCGGTGTCCCTCATCTGTCCGCTGGTGAAGATGCCGCTCTCC
 GTGCCCTGCGGGCAGAGACCTGCCACCTGCAGTGCTCGACGCCGCTTCTACCTGCAGATG
 AACCGAGAAGAACGCCACCTGGATGTGCCCGTGTGCAGAACGCCAGCCCCCTACGACCAGCTCATC
 ATCGACGGGCTCCTCTCGAAGATCCTGAGCGAGTGTGAGGACGCCAGAGATCGAGTACCTGGT
 GACGGCTCGTGGTGCCTGCGCCGATCCGCGCCAAAAGGAGCGCAGCTGCAGGCCAGGGGCCATC
 GTGCTGGGCCCTCGGACGCCAATGGGCTCTGCCGCCCGCAGCGTCAACGGAGCGGTGCCCTG
 GGCAGCACGGGTGGCGGCCGGCGGTGCCAGCATGGAGAATGGGAAGCCGGCGCCATGTGGT
 GACCTCACGCTGGACAGCTCATCGTCCCTCGGAGGATGAGGAGGAGGAAGAGGAGGAGGAAGAC
 GAGGACGAAGAGGGCCCCGCCAGGCCGCTGCCCTTCCAGAAGGCCCTGGTGCCTGCCCTGC

Figure 6 (continued)

>PIASy (prey)

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 GACTGTAGCCTGAGCTGTTCAAGAAGATCAAGGAGCTGTACGAGACCCGCTACGCCAAGAAGAAC
 TCGGAGCCTGCCCCACAGCCGACCGGCCCCCTGGACCCCTGACCATGCACTCCACCTACGACCGG
 GGG
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 CTTCAGGAGAGCCCGTGCATCTCGCATTGACGCCAAGACAGGTGGAGTTGATCCGGAACCTCCAGG
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 GGCTACTACCCCTCCAATAAGCCCGGG
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>PLIP

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Figure 6 (continued)

>PTN

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>PTPK

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>SETB1

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 CGCTTCCCCCTGGGTGGCTTCTTGCCAGCAAAGAATCCGGCTGGACAGAAACTTACTTGGGAC
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Figure 6 (continued)

>SH3GL3

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>SUMO-2

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 CTGGCAGGGCACAGTTTC

>SUMO-3

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>TALL

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 CTGGATGAGAAGTCTTCCGTTGGTTGCAACACGGAGCAGATGGCTGTGGAGAAGGCTCTGAC
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Figure 6 (continued)

>TCPG

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>VIM

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 GAA

Figure 6 (continued)

>VIMc

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>ZHX1

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Figure 6 (continued).

>ZNF33B

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Figure 6 (continued)

Nucleotide sequence data (fasta format)

>GDF9

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TGCACCTGTCGT
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>GAPD

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>MOV34

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Protein sequence data (fasta format)

>GDF9

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>GAPD

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MFVMGVNHEKYDNSLKIISNASCTNCLAPLAKVHDNFGIVEGLMTTVHAITATQKTVDGPSSKLWRDGRGALQ
NIIPASTGAAKAVGVKVIPELNGKLTGMAFRVPTANSVVVDLTCRLEPAKYDDIKKVVQKASEGPLKGILGYTEH
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>MOV34

Figure 6 (continued)

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LKLNPMTKHTDATMLFAELTYTLATEEAERIGVGDHVARMTATGSGENSTVAEHLIAQHSAIKMLHSRVKLILEYV
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I G R R M R G L F F

Figure 6 (continued)

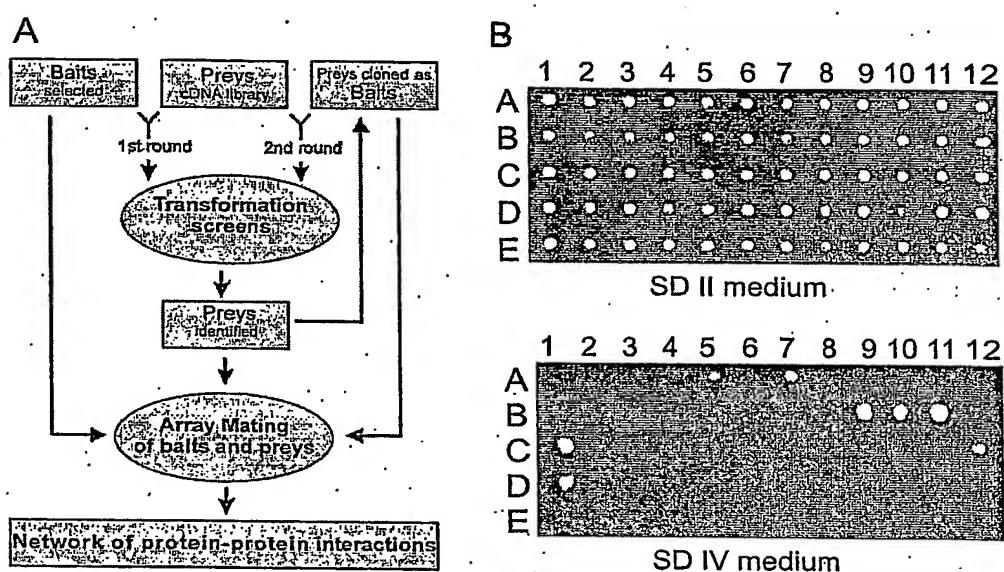
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Figure 7

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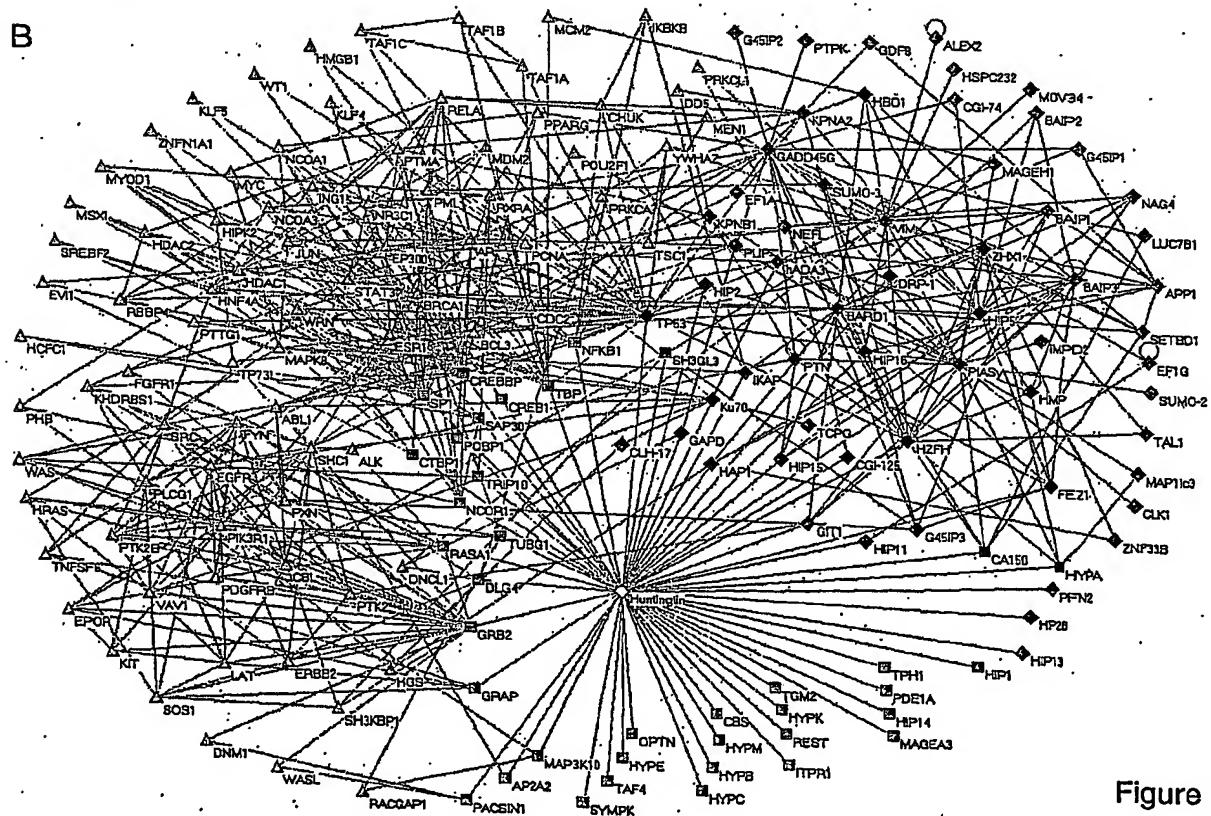
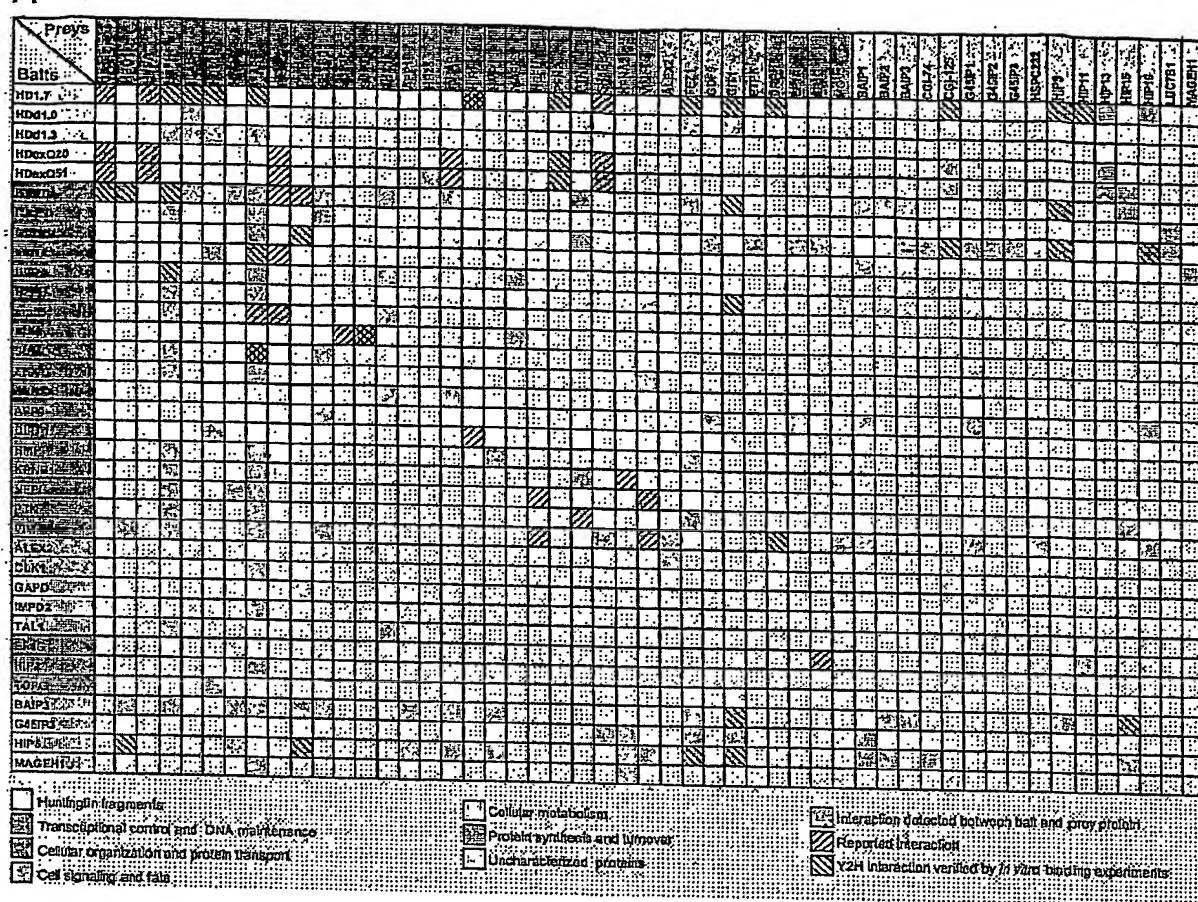


Figure 8

GST-fusion	pulled protein	beads + lysate	GST + lysate	GST-fusion + lysate	lysate only
CGI-125	HD510Q17	+++	+++	+++	+++
DRP-1	HD510Q17	+++	+++	+++	+++
FEZ1	HD510Q17	+++	+++	+++	+++
GIT1	HD510Q17	+++	+++	+++	+++
HZFH	HD510Q17	+++	+++	+++	+++
HIP11	HD510Q17	+++	+++	+++	+++
HIP1	HD510Q17	+++	+++	+++	+++
IKAP	HD510Q17	+++	+++	+++	+++
Ku70	HD510Q17	+++	+++	+++	+++
PFN2	HD510Q17	+++	+++	+++	+++
PIASy	HD510Q17	+++	+++	+++	+++
HIP5	HD510Q68	+++	+++	+++	+++
BARD1	GIT1	+++	+++	+++	+++
HIP5	GIT1	+++	+++	+++	+++
HZFH	GIT1	+++	+++	+++	+++
HIP15	BAIP3	+++	+++	+++	+++
GIT1	BAIP3	+++	+++	+++	+++
HIP5	HBO1	+++	+++	+++	+++
BARD1	HBO1	+++	+++	+++	+++
BARD1	HIP5	+++	+++	+++	+++
GADD45G	HIP5	+++	+++	+++	+++
SUMO-3	PIASy	+++	+++	+++	+++
hADA3	PIASy	+++	+++	+++	+++
HIP5	PLIP	+++	+++	+++	+++
GADD45G	PLIP	+++	+++	+++	+++
BARD1	CA150	+++	+++	+++	+++
BARD1	HZFH	+++	+++	+++	+++
GADD45G	HIP16	+++	+++	+++	+++
HZFH	HYPA	+++	+++	+++	+++
HIP5	FEZ1	+++	+++	+++	+++
CGI-125	GADD45G	+++	+++	+++	+++
DRP-1	VIM	+++	+++	+++	+++

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Figure 9

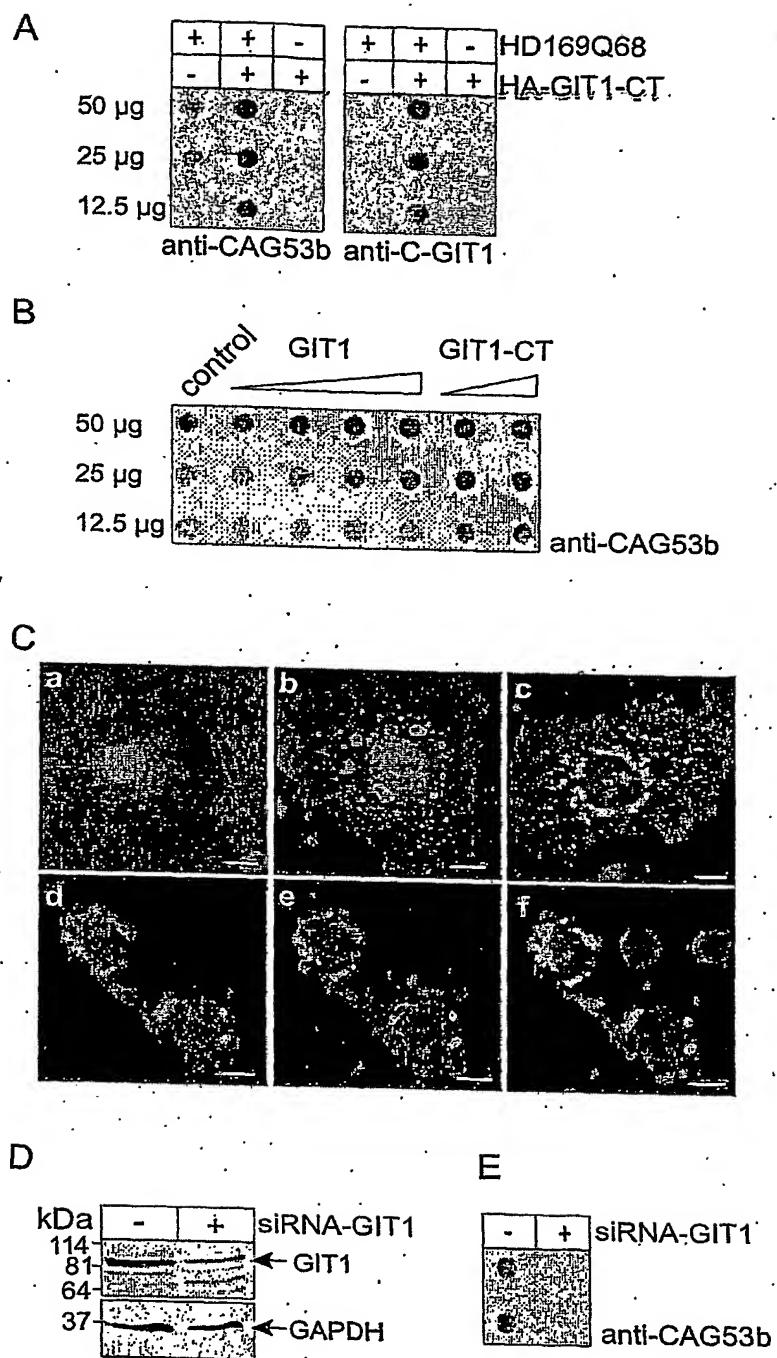


Figure 10

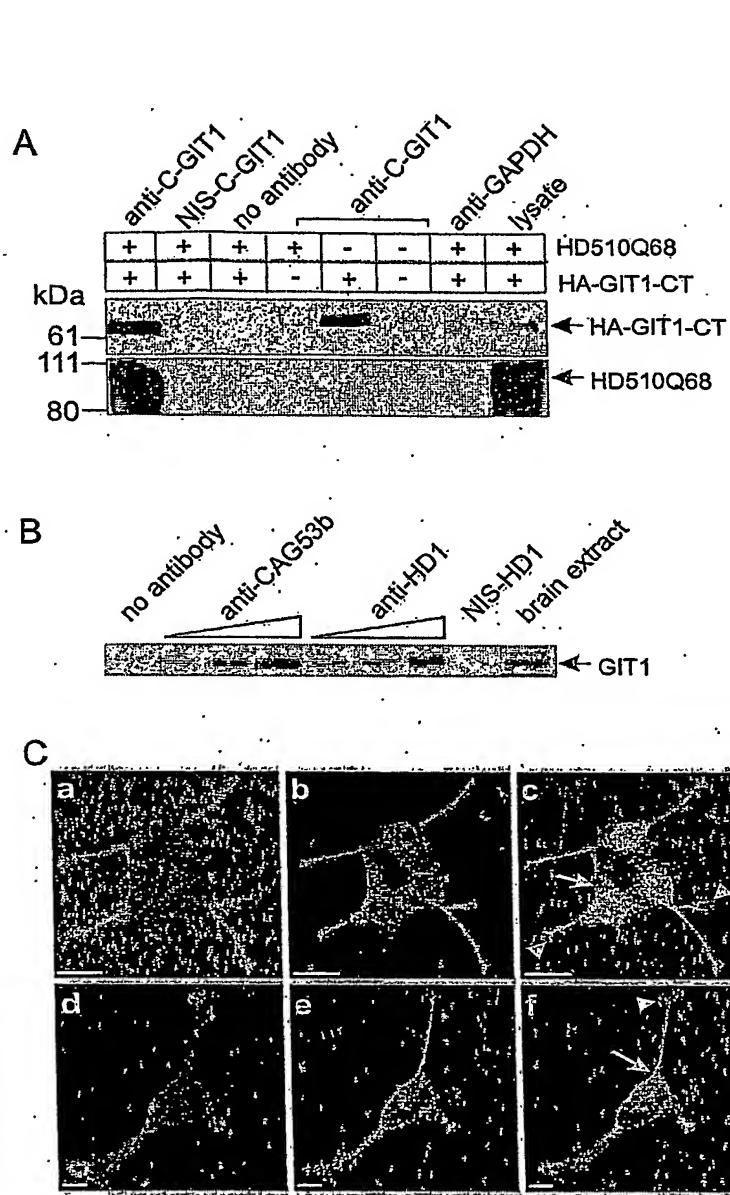


Figure 11

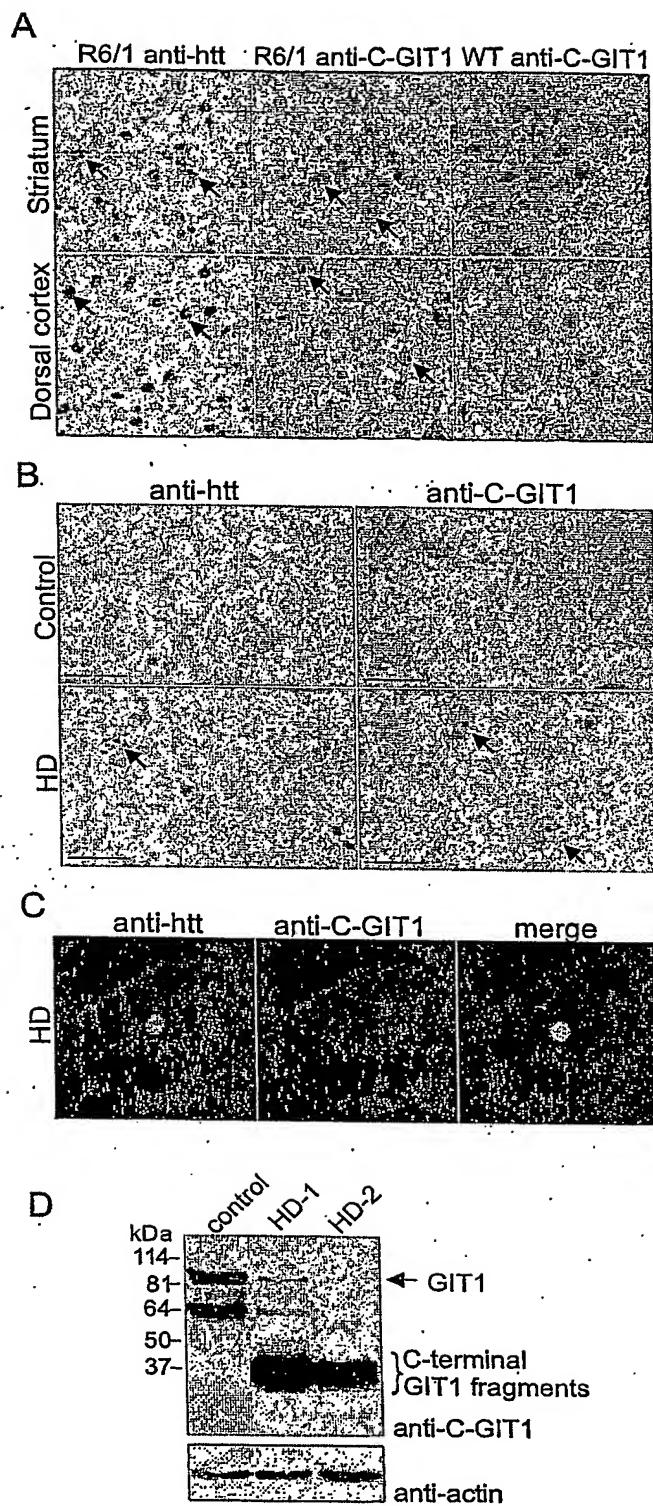


Figure 12

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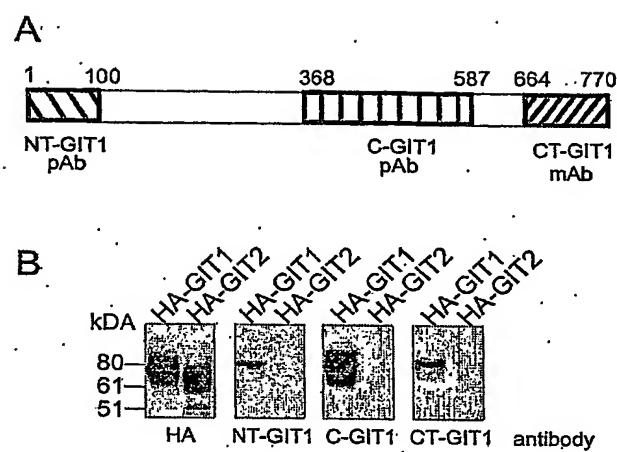


Figure 13